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                                                                            830 Primers useful for synthesizing in genetic manipulation.
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; 2000JP-00118774.
; 2000JP-00183765.
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Nagai
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K, Kojima
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S, Otsuki
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Matches 637;
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                                                                                                                 AGTTCAAGTAGCAACTATATCAAGGAAACATGTTCAACCAAATGGCAAAAGTGGGTGAAA
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Pred. No. 4.9e-137;
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30-JUN-2000; 2
03-AUG-2000; 2
21-SEP-2000; 2
27-SEP-2000; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                             microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-JAN-2001; 2001WO-US000670
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expression in human cervical epithelial cells.
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                                                                                                                                                                                                                                                             AAGCCAGCCCAGAAAAAGGGGGCAGAGACATGGTTTGATTCCTACGACTGTTCCAAATTTTG
                                                                                                                                                     ACTATACAAGAATATTTCTTTACAGTGGAGAACCTACTTATCTGGGAAATGAAACATCTG
                                                                                                                                                                                                         TGTTAAGGACCTTTAACAAGTTGGCTGAATTTTGGAGCAGAGTTCAAGAACATAGAAACCA
                                                                                                                                                                                                                                                                                                TGGCAAAGTGGGTGAAACAGGACAATGAAACAGGAATTTATTATGAGACATGGAATGTAA
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 TGATTGTGCACAAACAGTTCTATTTGTTTTATAATTTTTGAATATTGGTTTTTACCTATGA 1013
                                                     TCAAACCACATTTGCCAACTAAAGAATTTCTGTTGAGTCTCTTGCAAATTTTTGATGCAG
                                                                                                                                                                                                                                            AAGCCAGCCCAGAAAAGGGGGCAGAGACATGGTTTGATTCCTACGACTGTTCCAAATTTG
                                                                                                          TTTTTGGGCCAACAGGAAACAAGACTCTTGGTTTAGCCATAAAAAGATTTTATTACCCCT
                                                                                                                                     ACTATACAAGAATATTTCTTTACAGTGGAGAACCTACTTATCTGGGAAATGAAACATCTG
                                                                                                                                                                                        TGTTAAGGACCTTTAACAAGTTGGCTGAATTTGGAGCAGAGTTCAAGAACATAGAAACCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         invention relates to human single exon nucleic acid probes present sequence is one such probe. The SENPs are derived HeLa cells. The SENPs can be used to produce a single exon
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2000US-0207456P,
2000US-00608408,
2000US-00632366,
2000US-0234687P,
2000US-0236359P,
2000US-00024263.
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Pred. No. 2.4e-117;
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30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                                                          The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring ar displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                    WPI;
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                                         TGGCAAAGTGGGTGAAACAGGACAATGAAACAGGAATTTATTATGAGACATGGAATGTAA
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30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              genetic
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                     Human; gene expression; heart; microarray; vascular system; probe; cardiovascular disease; hypertension; cardiac arrhythmia;
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; 2000US-0207456P.
; 2000US-00608408.
; 2000US-00632366.
; 2000US-0234687P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                for gene expression analysis in human heart cell sample
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                                                                                                                                                         2001WO-US000666
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expression analysis; probe;

SEQ ID NO:

myeloma;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             measuring human gene expression in a sample derived from human heart. The present sequence is one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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100.0%; Pred. No. 2.4e-117;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancer such as lymphoma, leukaemia and myeloma. The present sequence is one of the probes of the invention
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21-SEP-2000;
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30-JUN-2000;
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                                         TCAAACCACATTTGCCAACTAAAGAATTTCTGTTGAGTCTCTTGCAAATTTTTTGATGCAG
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                       TCAAACCACATTTGCCAACTAAAGAATTTCTGTTGAGTCTCTTGCAAATTTTTTGATGCAG
                                                                                                               TTTTTGGGCCAACAGGAAACAAGACTCTTGGTTTAGCCATAAAAAGATTTTATTACCCCT
                                                                                                                                                            ACTATACAAGAATATTTCTTTACAGTGGAGAACCTACTTATCTGGGAAATGAAACATCTG
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                                                                                           TTTTTGGGCCAACAGGAAACAAGACTCTTGGTTTAGCCATAAAAAGATTTTATTACCCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 19549; 658pp + Sequence Listing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000US-0207456P.
2000US-00608408.
2000US-00632366.
2000US-023468P.
2000US-023468P.
2000US-0236359P.
2000GB-00024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000US-0180312P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 491; pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90 G; 152 T; 0 U; 0 Other;
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Mismatches

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Gaps

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773

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953 300 893 240 2.4e-117;

DB 4;

Length 494; Indels

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Matches 491
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26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-02343599.
04-OCT-2000; 2000GB-00024263.
                                                                                                                                                                        The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human probes which are derived from genomic sequences expressed in the luman brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-NOV-2001
                                                                                                                                                                                                                                                                                          Single exon nucleic acid
                                                                                                                                                                                                                                                                                                                  WPI; 2001-483446/52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-JAN-2001; 2001WO-US000667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; brain expressed exon; gene expression analysis; probe; microarray; Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAK19040 standard;
                                                                                                                         Sequence 494
                                                                                                                                                           epilepsy and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200157275-A2
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                                                                         al Similarity
491; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 brain expressed single exon probe SEQ
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AAGCCAGCCCAGAAAAAGGGGGCAGAGACATGGTTTGATTCCTACGACTGTTCCAAATTTG
                                               TGGCAAAGTGGGTGAAACAGGACAATGAAACAGGAATTTATTATGAGACATGGAATGTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCTCTGGTTTA 1084
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                       TGGCAAAGTGGGTGAAACAGGACAATGAAACAGGAATTTATTATGAGACATGGAATGTAA
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                                                                                                                                                                                                                                                                                                                                           Hanzel
                                                                                                                                                                                                                                                  SEQ ID NO 19031; 650pp + Sequence Listing;
                                                                           Conservative
                                                                                                                                                             cancers. The
                                                                                                                         BP; 170
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                                                                                                                                                                                                                                                                                                                                          DK,
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                                                                     45.3%; but
100.0%; Pr
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                                                                                                                         A; 82 C;
                                                                                                                                                                                                                                                                                                                                           Chen
                                                                                                                                                                                                                                                                                       probes for analyzing gene expression
                                                                                                                                                             present sequence
                                                                                                                                                                                                                                                                                                                                          Σ,
                                                                        Score 491; DB ;; Pred. No. 2.4 0; Mismatches
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                                                                                                                         90 G; 152
                                                                                                                                                                                                                                                                                                                                           Rank
                                                                                                                                                                                                                                                                                                                                           DR;
                                                                                                                         T; 0 U; 0 Other;
                                                                                    2.4e-117;
                                                                                                   DB 4;
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RESULT 13
ABS44658
ID ABS44658
AC ABS44
XX ABS46
COTON
XX Human
XX Homo
XX Homo
XX Homo
XX Homo
XX Homo
XX Homo
XX ABS46
PM 09-AU
XX 04-FB
PR 26-FB
PR 27-SB
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                                                                                                                                                                                                                                                                                          03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; single exon nucleic acid probe; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia; coronary heart disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                        26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                           04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human liver single exon probe, SEQ ID No 19648.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABS44658;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABS44658 standard; DNA; 494 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200157273-A2
                                                                                                                                                                                                                                               (MOLE-)
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                                                                    genome-derived single exon nucleic expression in human adult liver.
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                                                                                                                                                2001-488898/53.
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                                                                                                                                                                                                                                               MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCAAACCACATTTGCCAACTAAAGAATTTCTGTTGAGTCTCTTGCAAATTTTTGATGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AATTCCCTTTTATTAAAATAACATATGAAGAAATCCCTTTACCTATCAGAAACAAAACAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTTTTGGGCCAACAGGAAACAAGACTCTTGGTTTAGCCATAAAAAGATTTTATTACCCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACTATACAAGAATATTTCTTTACAGTGGAGAACCTACTTATCTGGGAAATGAAACATCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGTTAAGGACCTTTAACAAGTTGGCTGAATTTGGAGCAGAGTTCAAGAXCATAGAAACCA
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                                                                                                                                                                                            Hanzel
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2000US-0207456P.
2000US-0060840B.
2000US-00632366.
2000US-0234687P.
2000US-0236359P.
2000US-02036359P.
2000US-00024263.
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                                                                                                                                                                                            Chen W,
                                                                                                                                                                                              Rank
                                                                                                                                                                                              DR;
                                                                                                acid
                                                                                              probes
                                                                                                useful
                                                                                                     for
                                                                                                analyzing
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Claim 4;

SEQ ID NO 19648; 658pp; English

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RESULT 14
ABS19237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a single exon nucleic acid probe (SENP) (1) for measuring human gene expression in a sample derived from human adult liver, comprising one of 13109 defined nucleotide sequences given in the specification (or complements) fragments). The probe hybridises at high stringency to a nucleic acid molecule expressed in the human adult liver.
Human; ds; single exon probe; asthma; lung cancer; COPD; ILD chronic obstructive pulmonary disease; interstitial lung disfamilial idiopathic pulmonary fibrosis; neurofibromatosis; tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
                                                                                                                                     Human genome-derived single exon probe
                                                                                                                                                                                          19-AUG-2002
                                                                                                                                                                                                                                                                                                      ABS19237
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ftp.wipo.int/pub/published_pct_sequences
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Complements of the 1230 Open reaching frames derived from the 1230 Open reaching the movel set of probes controlled are a microarray comprising the novel set of probes collection of detectably labeled nucleic acids derived from human lung, comprising (a) contacting the array with a collection of detectably labeled nucleic acids derived from human lung measuring the label detectably bound to each probe of the carray; identifying exons in a eukaryotic genome, comprising (a) algorithmically predicting at least one exon from genomic sequences of the eukaryote; and (b) detecting specific hybridisation of detectably comprising (a) identifying exons from genomic sequences of the exaryotic; and to het probe the probe is included in the above mentioned microarray; assigning exons to a single exon probe, camprising (a) identifying exons from genomic sequence by the method comprising (a) identifying exons from genomic sequence by the method comprising (a) identifying exons from genomic sequence by the method comprising (b) measuring the expression of each of the exons in several conference in the exons should be assigned to a single gene, a pertide comprising one of 12011 sequences, mentioned in the specification, or encoded by the probes of the exons should be assigned to a single gene; a peptide comprising one conference obstructive pulmonary disease (CODD), interstitial lung cancer, chronic obstructive pulmonary disease (CODD), interstitial lung cancer, chronic obstructive pulmonary disease (CODD), interstitial lung disease (IID), familial idiopathic pulmonary fibrosis, neurofibromatosis, cuberous solutions, fibrocystic pulmonary haemosiderosis, pulmonary hypertension and hyaline membrane disease. The cuberous sequence is a single exon probe pen reading frame of the cuberous as expression and hyaline membrane disease. The cuberous expression and probe open reading frame of the cuberous as single exon part of the printed specification, but was obtained in electronic format directly from with the sequence is a figure tha
04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human lung comprising single exon nucleic acid probes having one 12614 nucleic acid sequences mentioned in the specification, or their complements or the 12387 open reading frames derived from the 12614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pulmonary histiocytosis; lymphangioleiomyomtosis; Karagener syndrome; pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia; primary ciliary dysplasia; primary ciliary dyskinesis; pulmonary hypertension; hyaline membrane disease; open reading frame; ORF.
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2000US-0207456P.
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Best Local Similarity
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                                   Jacobs K,
Spaulding
                                                                                                                                                                                                                                    Expressed sequence tag; secreted protein; haematopoiesis regulator; tissue growth; activin; inhibin; tumour invasion suppressor; EST; h chemotaxis; chemokinesis, haemostasis; gene therapy; thrombolysis; receptor; ligand; anti-inflammatory; tumour inhibitor; ds.
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             WPI; 1999-070078/06
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V, Agostino
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New polynucleotides encoding human secreted proteins - derived fr human blood, kidney, foetal lung, placenta, testes, brain, ovary, pituitary, retina and colon cDNA libraries.
                                                                                                                                          from
                                                                                                                                          e.g.
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Claim 1; Page 366; 641pp;

The present sequence represents an expressed sequence tag (BST), and is a polynucleotide of the invention. The polynucleotides of the invention are all secreted EST sequences isolated from a variety of human tissue sources. The EST sequences and proteins encoded by them are predicted to have useful biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional activity, immune stimulating or suppressing activity, haematopoiesis regulating activity, tissue growth activity, haemostatic activity, haemostatic chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, receptor/ligand activity, anti-inflammatory activity, cadherin/tumour invasion suppressor activity, tumour inhibition activity. The EST sequences are also stated to be useful for gene therapy

Sequence 506 BP; 171 A; 86 C; 119 G; 130 T; 0 U; 0 Other;

Ş 맔 S 밁 Ś В á 문 8 문 Ś 밁 Ś Matches 402; Query Match Best Local 159 339 279 677 **999** 797 737 459 99 Similarity CAAGTAGCAACTATATCAGGAAACATGTTCAACCAAATGGCAAAGTGGGTGAAACAGGAC GCTGAATTTTGGAGCAGAGTTCAAGAACATAGAAACCAACTATACAAGAATATTTCTTTAC GAGACATGGTTTGATTCCTACGACTGTTCCAAATTTGTGTTAAGGACCTTTAACAAGTTG GAGACATGGTTTGATTCCTACGACTGTTCCAAATTTGTGTTAAGGACCTTTAACAAGTTG CAAGTAGCAACTATATCAGGAAACATGTTCAACCAAATGGCAAAGTGGGTGAAACAGGAC ACTCTTGGTTTAGCCATAAAAAGATTTTATTACCCCTTCAAAC 899 AGTGGAGAACCTACTTATCTGGGAAATGAAACATCTGTTTTTGGGCCAACAGGAAACAAG AGTGGAGAACCTACTTATCTGGGAAATGAAACATCTGTTTTTGGGCCAACAGGAAACAAC GCTGAATTTGGAGCAGAGTTCAAGAACATAGAAACCAACTATACAAGAATATTTCTTTAC Conservative 37.0%; Pred. No. 4.7e-94; 0; Mismatches 1 Score 401.4; DB 2; Length Indels 0; Gaps 556 278 676 919 158 458 856 398 796 338 736 218

Search completed: April 22, Job time: 487.252 secs 2004, 00:39:08

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Title:
Perfect score:
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Listing first 45 summaries
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Pred. No. 25 the number of results predicted by chance to have

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

REFERENCE AUTHORS TITLE JOURNAL	LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE	RESULT BD07340		C 44 45	43	C 41		c 38	36	ი 35	· w	31 32	ωı	ი ი 29	ν.	o N	N	c 22	21	N F	c 18	16 17	. ــ	C 14	12	11	. 9	Ω 80 ~	3 D	OI H	4 (.	, 10, 1	1	Result No.
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1 (bases 1 to 4080)
Savukoski,M., Klockars,T., Holmberg,V., Santavuori,P., Lander,E.S and Peltonen,L.

CLN5, a novel gene encoding a putative transmembrane protein
                                                                                                                                                                                                                                                                                     Submitted (26-MAY-1998)
National Public Health:
                                                                                                                                                                                                                                                                                                                                                         2 (bases 1 to 4080)
Savukoski, M., Klocka
                                                                                                                                                                                                                                                                                                                           and Peltonen, L. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLN5, a novel gene encoding a putative transmembrane protein mutated in Finnish variant late infantile neuronal ceroid
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DRIGIN Query Match
Best Local Similarity
Matches 1069; Conserv 1803 1743 1683 1863 1623 1563 1443 2163 2103 2043 1923 1503 2283 1983 194 674 614 554 494 434 374 314 254 134 854 794 734 74 14 TTCCGTCCAAAACCTGATCCTTATTGTCAAGCTAAGTATACTTTCTGTCCAACTGGCTCA 253 TCCCGGGTCTCCGGGCATCCCCTCCCGGCGCCACTGGCCGGTGCCCTACAAGCGCCTTTGAC GACGCGCTTCCTGGTGCTGGGCGCTGGCGCTGCTTTGGCTCGCGGTTGGTTCCGGGCTGG GGGCAGGAGGTAGACACGGCACAGGGCGCGAGATGCGGCGGGGGCGCGGGCCCGGCTCGG GCAGAGACATGGTTTGATTCCTACGACTGTTCCAAATTTTGTGTTTAAGGACCTTTAACAAG GGCAACTGTACATTTCCCCCATCTCCGACCTGAAATGGATGCCCCCTTTCCTGGTGTAATCAA 493 TGGGAATTTAAATATGGAGACCTCCTGGGACACTTGAAAATTATGCATGATGCCATTGGA 1802 TGGGAATTTAAATATGGAGACCTCCTGGGACACTTGAAAATTATGCATGATGCCATTGGA TTCCGTCCAAAACCTGATCCTTATTGTCAAGCTAAGTATACTTTCTGTCCAACTGGCTCA GCGCAGGAGGTAGACACGGCACAGGGCGCCGAGATGCGGCGGGGGGGCGCGGCGCGCTCGG AAGACTCTTGGTTTAGCCATAAAAAGATTTTATTACCCCTTCAAACCACATTTGCCAACT AAGACTCTTGGTTTAGCCATAAAAAGATTTTATTACCCCTTCAAACCACATTTGCCAACT TACAGTGGAGAACCTACTTATCTGGGAAATGAAACATCTGTTTTTGGGCCAACAGGAAAC TACAGTGGAGAACCTTACTCTGGGAAATGAAACATCTGTTTTTTGGGCCAACAGGAAAC TIGGCTGAATTIGGAGCAGAGTTCAAGAACATAGAAACCAACTATACAAGAATATTICTT TTGGCTGAATTTGGAGCAGAGTTCAAGAACATAGAAACCAACTATACAAGAATATTTCTT GCAGAGACATGGTTTGATTCCTACGACTGTTCCAAATTTGTGTTAAGGACCTTTAACAAG GTTCAAGTAGCAACTATATCAGGAAACATGTTCAACCAAATGGCAAAGTGGGTGAAACAG GTTCAAGTAGCAACTATATCAGGAAACATGTTCAACCAAATGGCAAAGTGGGTGAAACAG GGCAACTGTACATTTCCCCATCTCCGACCTGAAATGGATGCCCCTTTCTGGTGTAATCAA TTCAGAAGTACATTAACTGGCAAGAACTACACAATGGAATGGTATGAACTTTTCCAACTT TTCAGAAGTACATTAACTGGCAAGAACTACACAATGGAATGGTATGAACTTTTTCCAACTT CCTATCCCAGTTATGGAGGGTGATGATGACATTGAAGTTTTTCGATTACAAGCCCCAGTA 1742 CCTATCCCAGTTATGGAGGGTGATGATGACATTGAAGTTTTTCGATTACAAGCCCCCAGTA 313 TCCCGGGTCTCGGGCATCCCCTCCCGGCGCCACTGGCCGGTGCCCTACAAGCGCTTTGAC Conservative 98.5%; Score 1067.8; DB 9; Pred. No. 7.7e-235; 0; Mismatches 2; Indels Length 0; Gaps 553 1922 16.62 373 1682 1502 2342 2282 2222 2162 2102 2042 1622 193 1562 913 853 793 733 673 613 433 133 73 0

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374 TTC	Qy 314 TGGGAATTTAAATATGGAGACCTCCTGGGACACTTGAAAATTATGCATGATGCCATTGGA 373	QY 254 CCTATCCCAGTTATGGAGGGTGATGATGATTTTTCGATTACAAGCCCCAGTA 313	Oy 194 TTCCGTCCAAAACCTGATCCTTATTGTCAAGCTAAGTATACTTTCTGTCCAACTGGCTCA 253	Qy 134 TCCCGGGTCTCCGGGCATCCCCTCCCGGCGCGCACTGGCCCTACAAGCGCTTTGAC 193	Qy 74 GEACGECETTCCTGGTGCTGGGCGCTGCTTTGGCTCGCGGTGGTTCCGGGGCTGG 133	gggcaggaggtagacacggcachagggcgccgagatgcggcgggggcgcggggcgcggggcgcggggcgcggggcgc	Query Match 98.2%; Score 1064.6; DB 6; Length 2120; Best Local Similarity 99.6%; Pred. No. 3.5e-234; Matches 1067; Conservative 0; Mismatches 4; Indels 0; Gaps 0;	/org/mol/db/	Location/Qualifiers (16)(1089). Location/Qualifiers 1. 2120	C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/PC 10, PC C12P21/02,C12Q1/68//C12P21/08,G06F17/30,C12N15/00,C12N5/00 CC Primer for synthesizing full-length cDNA and use thereof FH Key	PI YÜRI KAWAI,AI WAKAMATSU,TOMOYASU SUGIYAMA,KEIICHI NAGAI, PI SHINICHI KOJIMA, PI TETSUJI OTSUKI,HISASHI KOGA PC	PD 22-JAN-2002 PF 07-JUL-2000 JP 2000253172 PF TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAYASHI, SHIZUKO	JOURNAL PACENT: UP 2002017375-A 3289 22-JAN-2002; HELIX RESEARCH INSTITUTE COMMENT OS Homo sapiens (human) DN .TD 2002017375-A 17289	Ota, T., Nis Wakamatsu, A Koga, H.	4 Hom Euk Mam	7858.1 GI:23222803 7858.17375-A/3289.	BD127858

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Homo sapiens cDNA FLJ90628 fis, clone PLACE1003
to Homo sapiens putative transmembrane protein
Direct Submission
Submitted (25-MAR-2002) Takao Isogai, Helix Research Institute,
Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Jap
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Isogai, T. and Otsuki, T.
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                                                                      human cDNA sequencing
                                                                      project
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(B-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) Numan cDNA sequencing project supported by Ministry of Reconomy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA full insert sequencing: Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center; CDNA 5'-& 3'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.).
                                                                        GCAGAGACATGGTTTGATTCCTACGACTGTTCCAAATTTGTGTTAAGGACCTTTAACAAG
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/db_xref="taxon:9606"
/clone="PLACE1003407"
/tissue_type="placenta"
/clone_lib="PLACE1"
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Matches 640; Conserv
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patent: JP 2001511
ZYMOGENETICS INC
OS ARTIFICIAL SE
PN JP 2001511345
PD 14-AUG-2001
PF 24-JUL-1998 U
PR 24-JUL-1997 V
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CC Degenerate nucleotide sequence encoding zsig46 polypeptide CC SEQ ID NO:2 FH Key 1. .1038 FT source 1.038 /organism='Artificial Sequence'.
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JP 2001511345-A/12.
synthetic construct
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24-JUL-1998 JP 2000504249
24-JUL-1997 US 60/053613
PAUL O SHEPPARD, DIBRA G GILBERTON
C12N15/09, A61K38/00, A61K48/00, C07K14/47, C07K16/18,
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                                                                                                                                                                             /organism="synthetic construct"
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/db_xref="taxon:32630"
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                                                                                                                71.3%; Score 772.4; DB 6; 61.7%; Pred. No. 5.2e-167; tive 232; Mismatches 165;
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Mus musculus ceroid-lipofuscinosis, IMAGE:5251891), partial cds.
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AUTHORS
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TITLE
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Klausher, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences

P. 2018 8257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: nisc_mgc@nhgri.nih.gov

Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                        Series: IRAK Plate: 56 Row: c Column: 7
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF
                                                                                                                                                                                                                                                                                                                                                                                                                     Clone distribution: MGC clone distribution through the I.M.A.G.E. Consortium/LINL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tissue Procurement: Lothar Hennighausen Ph.D., Robin Hump
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (06-MAR-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strausberg, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus
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                        /tissue_type="Mammary tumor.
old, gross tissue."
/clone_tib="NCI_GCAP_Mam5"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                              /db_xref="taxon:10090"
/clone="IMAGE:5251891"
                                                                                                                                                                                                                                      organism="Mus musculus"
                                                                                                                                                                            strain="C57BL/6J"
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Rodentia;
pCMV-SPORT6"
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                                                                                                     WAP-TGF alpha model.
                                                                                                                                                                                                                                                                                                                                                                                                                     http://image.llnl.gov
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VVATISGNTFNKVAEWVKQDNETGIYYETWTVRAGFGQGAQTWFESYDCSNFVLRTYK
KLAEFGTEFKKIETNYTKIFLYSGEFIYLGNETSIFGPKGNKTLALAIKKFYGFFRPY
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/db_xref="MGI:2442253"
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/taanslation="TREAHMRPALALALLGLATILGASPTSGQRWPVDYKRESERPKT
/translation="TREAHMRPALALALLGLATILGASPTSGQRWPVDYKRESERPKT
DPYCQAKYTFCPTGSPIPVMKDNDVIEVLRLQAPIWEFKYGDLLGHFKLMHDAVGFRS
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/protein_id="AAH25487.1"
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Allen(C., Allen, H., Labrooks, S., Amin, A., Angulano, C., Alder, H., Abbrooks, S., Amin, A., Angulano, D., Alder, H., Abbrooks, S., Amin, A., Angulano, D., Bardaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Barch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, J., Ceasar, H., Calderon, E., Checko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chen, Z., Chen, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D., Soura, I., Davila, M.I., Davis, C., Davy, Carroll, L., De Anda, C., Dederich, D., Davis, G., Davy, Carroll, L., De Anda, C., Dederich, D., Davis, G., Davy, Carroll, L., De Anda, C., Dederich, D., Davis, G., Davy, Carroll, M., Durbin, K., Duval, B., Eaves, K., Belaga, A., Escotto, M., Engene, C., Evans, C.A., Falls, T., Fan, G., France, C.M., Gabisi, A., Ganta, R., Garcia, A., Garrer, T., Garza, M., Gunaratne, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Johnson, R., Johnson, R., Johnson, E., Krapathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kowis, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Liz, Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., London, P., Longacre, S., Lopez, J., Mansharine, S., McLeod, M.P., Mortis, S., Munidasa, M., Murphy, M., Nair, L., Martin, R., Partis, S., Paul, H., Perez, A., Perez, A., Perez, A., Perez, B., Pu, L.-L., Plags, F., Pulazo, M., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Sanders, S., Sanders, S., Reigh, R., Sanders, S., Sanders, S., Scott, G., Shatsman, S., Shen, H.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Muzny,D.Marie., Metzker,M.Lee., Abramzon,S., Adams,C., Alder,J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus
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3. *** SEQUENCING IN PROGRESS
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JOURNAL
                                                                                                         Submitted (11-OCT-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Oct 11, 2002 this sequence version replaced gi:21738217.
On Oct 11, 2002 this sequence version replaced gi:21738217.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-Scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome
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Rat Genome Sequencing Consortium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (05-FEB-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
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                                                                         shotgun sequence only contigs will be indicated in the feature
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Genome Center
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COMMENT

JOURNAL TITLE AUTHORS

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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft_data.)
NOTE: This is a "working draft' sequence. It currently consists of 1 contigs. Gaps between the contigs is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

1 198524: contig of 198524 bp in length. are represented as runs of N. The order of the pieces Assembly program: Phrap; version 0.990329
Consensus quality: 177481 bases at least Q40
Consensus quality: 19640 bases at least Q30
Consensus quality: 181141 bases at least Q20
Estimated insert size: 183954; sum-of-contigs estimation Center clone name: CH230-331D3 Center: Baylor C Center code: BCM Quality coverage: 6x in Q20 bases; sum-of-contigs estimation /clone="CH230-331D3" /mol_type="genomic DNA" /db_xref="taxon:10116" Location/Qualifiers organism="Rattus norvegicus" .198524 College of Medicine data.html)

FEATURES

misc_feature

/note="wgs end extension clone_end:T7" misc_feature 131409131443 /note="clone_boundary clone_end:T7	
Bequence:RXAPC14 370198217 Se="clone boundar ne end:Sp6 s:Mbol	
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Query Match 61.1%; Score 662.8; DB 2; Length 198524; Best Local Similarity 77.0%; Pred. No. 3.4e-141; Matches 808; Conservative 0; Mismatches 242; Indels 0; Gaps 0;	
Db 38682 CGACGCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	
90 GCTGGGCGCTGGCGTTTGGCTCGCGGTGGTTCCGGGGTCGGTTCCGGGTTCTCGGGTC	
38622 ACTGGCGCCAGGCGCTCGCGCTACTGGGGCGACTCTGGGGCGCTCCC 38	
Y 150 TCCCCTCCCGGCGCCACTGGCCGGTGCCCTACAAGCGCTTTGACTTCCGTCCAAAACCTG 209	
210 ATCCTTATTGTCAAGCTAAGTATACTTTCTGTCCAACTGGCTCACCTATCCCAGTTATGG 269	
w	
389	
38382 GAGACCTCCTGGGACACTTCAAAATCATGCACGATGCCATTGGATTCAGGAGTACGCTGA 38	·
390 CIGGCAAGAACTACACHAIGSAAIGGTAIGAACTITTCCAACTITGGCAACTGTACATTTC 449 5	<u>-</u>
39 450 CCCATCTCCGACCTGAAATGGATGCCCCTTTCTGGTGTAATCAAGGGCTGCCTGC	
2y 510 TTGAGGAATTGATGATGATGACTAGCAAATGAGAAATGAGTAGTAGTAGAACTA 569	
Y 570 TATCAGGAAACATGTTCAACCAAATGGCAAAGGTGAAACAGGACAATGAAACAGGAA 629	
Y 630 TITATTATGAGACATGGAATGTAAAAGCCAGCCCAGAAAAGGGGGCAGAGACATGGTTTG 689	
Y 690 ATTCCTACGACTGTTCCAAATTTGTGTTAAGGACCTTTAACAAGTTGGCTGAATTTGGAG 749	
Y 750 CAGAGTICAAGAACATAGAAACCAACTATACAAGAATATITTCTTTACAGTGGAGAACCTA 809	
Y 810 CTTATCIGGGAAATGAAACATCIGTTITIGGGCCAACAGGAAACAAGACTCTTGGTTTAG 869	

RESULT 9 AC107510 AC1	Db 37662 CTT	Qy 1050 CTT	Db 37722 TTC	Oy 990 TTC	Db 37782 ATT	QY 930 GTC	Db 37842 CC	Qy 870 CCJ
CON ACIOTSIO 227920 bp DNA linear HTG 13-MAY-2003 ***********************************	CTTTACCTACCCAACATACGACATTTACCG 37633	CTTTACCTATCAGAAACAAAACACTCTCTG 1079	TIGAGTATIGGTTICTACCTATGAAACCCCCCTTTGTCAAAATAACGTACGAGGAAACCC 3766	TIGAATATIGGTTITTACCTATGAAATTCCCTTTTATTAAAATAACATATGAAGAAATCC 1049	ATTICTIGAAAATTITTGACACAGTGATTATGCACAGAGAGTTCTACCTGTTTTATAACT 37723	GTCTCTTGCAAATTTTTGATGCAGTGATTGTGCACAAACAGTTCTATTTGTTTATAATT 989	CCATAAAAAAATTTTACGGCCCCGTCAAACGGTATTCGTCAACCAAAGATTTTCTGTTGA 37783	CCATAAAAAGATTTTATTACCCCTTCAAACCACATTTGCCAACTAAAGAATTTCTGTTGA 929

Indels Length

89

0;

227920; 0 Gaps

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                                                                                    source
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On May 13, 2003 this sequence version replaced gi:22855855.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome storgun sequence only contigs will be indicated in the feature
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                                                                                                                                                                                                                                                                                                                                                                                                 NOTE: Estimated insert size may differ from sequence length (see http://www.hsgsc.bcm.tmc.edu/docs/Genbank_draft_data.html) (NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
                                                                                                                                                                                                                                                                                                                                              as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center project name: GJBR
Center clone name: CH220-138J6
Center clone name: CH220-138J6
Center clone name: CH220-138J6
Center clone name: Atlas 3.0;
Assembly program: Atlas 3.0;
Consensus quality: 214528 bases at least Q40
Consensus quality: 217034 bases at least Q20
Consensus quality: 219064 bases at least Q20
Estimated insert size: 223690; sum-of-contigs estimation
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Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                              223660
224739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                      224839
                                                                                                                                                                                                                                                                                        223560
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.er: Baylor College of Medicine
/organism="Rattus norvegicus"
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                                                                                                               Location
                                                                                       .227920
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Matches 775;
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                              GTCTCTTGCAAATTTTTTGATGCAGTGATTGTGCACAAACAGTTCTATTTGTTTTATAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATCCTTATTGTCAAGCTAAGTATACTTTCTGTCCAACTGGCTCACCTATCCCAGTTATGG 269
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                                                                                    CCATAAAAAATTTTACGGCCCCGTCAAACGGTATTCGTCAACCAAAGATTTTCTGTTGA
                                                                                                                                                                                                      TTTACTTGGGAAATGAAACGTCTATTTTTGGGCCCAAAGGAAACAAGACCCTTGCTTTGG
                                                                                                                                                                                                                                             CTTATCTGGGAAATGAAACATCTGTTTTTGGGCCAACAGGAAACAAGACTCTTGGTTTAG 869
                                                                                                                                                                                                                                                                                                                         CAGAATTCAAGAAGATAGAAACAAACTATATGAAAATATTTCTTTACAGCGGAGAACCGA
                                                                                                                                                                                                                                                                                                                                                       CAGAGTTCAAGAACATAGAAACCAACTATACAAGAATATTTCTTTACAGTGGAGAACCTA 809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTCCTACGACTGTTCCAAATTTGTGTTAAGGACCTTTAACAAGTTGGCTGAATTTGGAG 749
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCCACCTTCGGCCGGAAGTGAACGCTCCGTTCTGGTGTAACCAGGGGGCAGCCTGCTTCT
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                                                                                                                                             CCATAAAAGATTTTATTACCCCTTCAAACCACATTTGCCAACTAAAGAATTTCTGTTGA 929
                                                                                                                                                                                                                                                                                                                                                                                                                                     AATCCTACGACTGTTCGAATTTTGTCTTAAGGACATATGAGAAATTGGCTGAATTTGGAA 3792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTTATTACGAGACATGGACAGTCCGGGCCAGCCCAGGAAAAGGGGCGCAGACATGGTTTG 37861
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37501

37441

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37321

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Db Qy	g V	gb Qy	Qy Db	gb Qy	Query Match Best Local Matches 63	ORIGIN	FEATURES source					COMMENT	TITLE JOURNAL	AUTHORS	REFERENCE	VERSION KEYWORDS SOURCE ORGANISM		RESULT 10		Db 38
254 CCTATCCCAGTTATGGAGGGTGATGATGACATTGAAGTTTTTCGATTACAAGCCCCAGTA 3:3	194 TICCGTCCAAAACCTGATCCTTATTGTCAAGCTAAGTATACTTTCTGTCCAACTGGCTCA 253	134 TCCCGGGTCTCGGGCATCCCCTCCCGGCGCCACTGGCCGGTGCCCTACAAGCGCTTTGAC 193	74 GGACGCGCTTCCTGGTGCTGGGCGCTGGCGCTGGCTTTGGCTCGCGGTGGT	14 GGGCAGGAGGTAGACACGGCACAGGGCGCCGAGATGCGGCGGGGGGGG	/ Match 52.3%; Score 567; DB 6; Length 697; Local Similarity 95.2%; Pred. No. 8.9e-120; les 637; Conservative 0; Mismatches 24; Indels 8; Gaps 5;	πρ/ mc/ oo/		Cl2P21/02,Cl2Q1/68/ mer for synthesizing Location/Qual	2N1 0,	INI	PF 07-JUN-2000 JP 2000253172 PI TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAYASHI, SHIZUKO	HELLA KESEARCH INSTITUTE OS Homo sapiens (human) PN JP 2002017375-A/618 Ph 22-TAN-2002	Primer for synthesizing full-length cDNA and use thereof Primer for 2002017375-A 618 22-JAN-2002;	Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y., Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and		BD125187.1 GI:23220132 JP 2002017375-A/618. Homo mapiens (human)		38182 IIGAGIAIIGGITICTACCTAIGAAACCCCCCTTTGTCCTGCTAAGA 38208	TTGAATATTGGTTTTTACCTATGAAATTCCCCTTTTATAAAATAACA	38102 ATTTCTTGAAAATTTTTGACACAGTGATTATGCACAGAGAGTTCTACCTGTTTTATAACT 38161
ORIGIN Query Matc Best Local	rearures source					TITLE JOURNAL COMMENT	AUTHORS	ORGANISM	VERSION KEYWORDS SOURCE	LOCUS DEFINITION ACCESSION	RESULT 11	Qy Db			B 8	Qy Db	Qy Db	Дb		VΩ
/db_xrei="taxon:9606" h 52.3%; Score 567; DB 6; Le Similarity 95.2%; Pred. No. 8.9e-120;		Location/Qualifiers 1. 697 /organism='Homo sapiens (human)'.	C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/ PC 10, C12P21/02,C12Q1/68//C12P21/08,G06F17/30,C12N15/00,C12N5/00 CC PC C12P21/02,C12Q1/68//C12P21/08,G06F17/30,C12N15/00,C12N5/00 CC PC	PI YURI KAWAI,AI WAKAMATSU,TOMOYASU SUGIYAMA,KEIICHI NAGAI, PI SHINICHI KOJIMA, PI TETSUJI OTSUKI,HISASHI KOGA	PN JP 2002017375-A/1884 PD 22-JAN-2002 PF 07-JUL-2000 JP 2000253172 PI TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAYASHI, SHIZUKO PI TOHIT	Primer for synthesizing full-length cDNA and use thereof Patent: JP 2002017375-A 1884 22-JAN-2002; HELIX RESEARCH INSTITUTE OS Homo sapiens (human)	<pre>L (Dases I CO 897) Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y., Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and Koga,H.</pre>	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	BD126453.1 GI:22221398 JP 2002017375-A/1884. Homo sapiens (human)	BD126453 697 bp DNA linear PAT 18-SEP-2002 Primer for synthesizing full-length cDNA and use thereof. BD126453		666 AAAAGGGGG 674 	19 CAAGGACAA	1 CAGGACAATGAAACAGGAATTTATTATGAGACATGGAATGTAAAAGCCCAGCCC	553 AGTTCAAGTAGCAACTATATC-AGGAAACATGTTCAACCAAATGGC-AAAGTGGGTGAAA 610 	494 GGCGCTGCCTTTTTTGAGGGAATTGATGATGTTCACTGGAAGGAA	434 GGCAACTGTACATTTCCCCATCTCCGACCTGAAATGGATGCCCCTTTCTGGTGTAATCAA 493 	374 TTCAGAAGTACATTAACTGGCAAGAACTACACAATGGAATGGTATGAACTTTTCCAACTT 433	19 TGGAATTTAAATATGGAGACCTCCTGGGACACTTGAAAATTATGCATGC	314 TGGGAATTTAAATATGGAGACCTCCTGGGACACTTGAAAATTATGCATGATGCCATTGGA 373

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2 (bases 1 to 106988)

Hawkins, T.L., Reeve, M.P., Christoffersen, A., Birren, B.W.,
Fasman, K.H., Lander, E.S., McKernan, K., Munro, C., Richardson, P.,
Barna, N., Brown, K., Cooke, P., Daly, M.J., Forreet, C., Fripp, W.J.,
Barna, N., Geraigery, K., Hagos, B., Jacotot, L., Lane, M., MacKenzie, J.,
Gage, D., Geraigery, K., Hagos, B., Jacotot, L., Lane, M., MacKenzie, J.,
Marquis, N., McDermott, J., Moloney, N., Morrow, J., Nachman, A.,
                                                                                                                                                            1 (bases 1 to 106988)
Hawkins, T.L., Reeve, M.P., C.
Fasman, K.H. and Lander, E.S.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae
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Genomic sequence from Human 1
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Hawkins, T.I., Reeve, M.P., Christoffersen, A., Birren, B.W., Fasman, K.H., Lander, E.S., McKernan, K., Munro, C., Richardson, P., Barna, N., Chang, A., Cooke, P., Daly, M.J., Forrest, C., Fripp, W.J., Gage, D., Geraigery, K., Hagos, B., Jacotot, L., Lane, M., MacKenzie, J., Marquis, N., McDermott, J., Molney, N., Morrow, J., Nachman, A., Naylor, J., O'Connor, T., Peterson, K., Rollins, G., Spencer, J., Naylor, J., Stone, C., Strickland, C., Sydney, K., Wilmer, F. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          All repeats were identified using RepeatMasker: Smit, A.F.A. Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (29-MAY-1997) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On May 29, 1997 this sequence version repaired gi:1932720. The Staden databases, finishing information, and all chromatographic files used in the assembly of this clone are available from our anonymous ftp site.
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Direct Submission
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. 42848 family="L1MB8" . 43151 family="AluJb" 43318 43318 family="L1MA10"	. 4.1003 family="LIPA2"42352 family="MLTIE" .42771 family="AluSq"	manily="Allux" _ement(3643736461) _family="AT_rich" _fement(3996740261) _family="Allux" _family="Allux" _ement(4074140915) _family="Allux" _family=	munity="MIR" [-maily="MIR" [-maily="MIR" [-maily="AllJo" [-maily="AllJo" [-maily="MIR" [-maily="MIR" [-maily="MIR" [-maily="MIR" [-maily="MIR" [-maily="AllJox" [-maily="MIR" [-maily="	<pre>Lamily="MIRZ" lement(2717, .28532) family="L1PB1" fement(28553, .28854) family="Aluag" lement(2860, .29076) family="L1" fement(2860, .29561)</pre>	<pre>f21534 f.amily="AluSx" family="A33123353) family="GC_rich" lement (2354623578) family="GC_rich" f24707 family="MIR" f24707</pre>	ame ame	<pre>family="AluJo" .9946 .1994</pre>
QY 988 TITTGAAFATTTGATTTAACTATGAAATTCCCTTTTATTAAAATAACATATGAAGAAAT 1047	Db 32159 AGCCATAAAAGATTTTATTACCCCTTCAAACACATTTGCCAACTAAAGAATTTCTGTT 32218 Oy 928 GAGTCTTGCAAATTTTTGATGCAGTGATTGTGCACAAACAGTTCTATTTGTTTTATAA 987	808 TACTTATCTGGGAAATGAAACATCTGTTTTTGGGCCAACAGGAAACAAGACTCTTGGTTT 32099 TACTTATCTGGGAAATGAAACATCTGTTTTTTTGGGCCAACAGGAAACAAGACTCTTGGTTT 32099 TACTTATCTGGGAAATGAAACATCTGTTTTTTGGGCCAACAGGAAACAAGACTCTTGGTTT 868 AGCCATAAAAGATTTTATTACTGCCCTTCAAACCACATTTGCCAACTAAAGAATTTCTGTT	Db 31919 AATTTATTATGAGACATGGAATGTTAAAGGCCAGCCCAGAAAAGGGGGCAGAGACATGGTT 31978 688 TGATTCCTACGACTGTTCCAAAATTTGTGTTAAAGGACCTTTAACAAGTTGGCTGAATTTGG 747	Similarity 99.4%; Pred. No. 1.3e-106; 4; Conservative 0; Mismatches 3; TATATCAGGAAACATGTTCAACCAAATGGCAAAGTGGGTGA [/rpt_family="MIR _region complement (54533 /rpt_family="(TG/ region complement (54580 /rpt_family="Aluoregion complement (54755) _region complement (54755) /rpt_family="(CA) 47.3%; Scol	region region region	repeat_region 4325343427 /rpt_family="L1MB8" repeat_region /rpt_family="L1MB8" repeat_region complement(4418844481) /rpt_family="N1MS6" repeat_region 4454445246 /rpt_family="N1TR8" repeat_region complement(4699947032) /rpt_family="NT_rich" repeat_region complement(4741147431) /rpt_family="NT_rich" repeat_region complement(4761247684) /rpt_family="(ATRA)n" repeat_region complement(4794648239) /rpt_family="N1MS6448239) /rpt_family="N1MS6448239) /rpt_family="N1MS6448239) /rpt_family="N1MS6448239) /rpt_family="N1MS6448239)

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Submitted (10-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire,
Submitted (10-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk
On Sep 8, 2000 this sequence version replaced gi:6982057.
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AL136440.2 GI:10039473
HTG; HTGS_PHASE1; HTGS_CANCELLED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Assembly program: XGAP4; version 4.5 Sequencing vector: plasmid; L08752; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Consensus quality: 162085 bases at least Q40 Consensus quality: 164521 bases at least Q30 Consensus quality: 166040 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Insert size: 168062; sum-of-contigs
Insert size: 164996; 1.7% error; agarose-fp
Quality coverage: 4.08x in Q20 bases; sum-of
coverage: 4.16x in Q20 bases; agarose-fp
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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AGCAGAGTTCAAGAACATAGAAACCAACTATACAAGAATATTTCTTTACAGTGGAGAACC
                                                                TGATTCCTACGACTGTTCCAAATTTGTGTTAAGGACCTTTAACAAGTTGGCTGAATTTGG
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/db_xref="taxon:9606"
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Pred. No. 1.5e-3;
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Homo sapiens chromosome 13 clone RP11-453N22,
AL359875.3 GI:9864777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (12-JUN-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Aug 22, 2000 this sequence version replaced gi:8894433.
                                                                                                                                                                                                                                                                                                                                                                                                   Insert size: 245987; sum-of-contigs
Insert size: 19096; agarose-fp
Quality coverage: 2.52x in Q20 bases; sun
coverage: 3.92x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Assembly program: XGAP4; version 4.5 Sequencing vector: plasmid; LO8752; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Consensus quality: 220597 bases at least Q40 Consensus quality: 234299 bases at least Q30 Consensus quality: 241103 bases at least Q20 Insert size: 245987; sum-of-contigs
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Center code: SC
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Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: humquery@sanger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Web site:
                                                                                                                                                   runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TACTTATCTGGGAAATGAAACATCTGTTTTTGGGCCAACAGGAAACAAGACTCTTGGTTT
                                                                                                                                                                                                                                                                                         NOTE: This is a 'working draft' sequence. It currently consists of 53 contigs. The true order of the pieces is not known and their order in this sequence record is
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22, 53 unordered pieces.
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="13"
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                                             Jacobs K., McCoV,J.M., Lavallie,E.R., Racie,L.A., Me
Treacy,M., Spaulding,V. and Agostino,M.J.
Secreted expressed sequence tags (sESTs)
Patent: JP 2001518793-A 825 16-OCT-2001;
GENETICS INSTITUTE INC
PN JP 2001518793-A/825
PD 16-OCT-2001
PF 10-APR-1998 JP 1998543070
PR 10-APR-1997 US 08/837312
PI KENNETH JACOBS,JOHN M MCCOY,EDWARD R LAVALLIE,L
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JP 2001518793-A/825.
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BD060465
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PI MAURICE TREACY, VIKKI SPAULDING, MICHAEL J AGOSTINO PC C12N15/12, C12N5/10, C07K14/47, C12Q1/68, A61K38/17 CC Strai
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                                  DAVID MERBERG,
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                                               JP 2001518793-A/825
16-OCT-2001
10-APR-1998 JP 1998543070
10-APR-1997 US 08/837312
KENNETH JACOBS, JOHN M MCCOY, EDWARD R LAVALLIE, LISA A
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CC Top
FH Key
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                                                                       ACTCTTGGTTTAGCCATAAAAAGATTTTATTACCCCTTCAAAC 899
                                                                                                                            AGTGGAGAACCTACTTATCTGGGAAATGAAACATCTGTTTTTGGGCCAACAGGAAACAAG 856
                                                       ACTOTTGGTTTAGCCATAAAAAGATTTTATTACCCCTTCAACC 501
                                                                                                             AGTGGAGAACCTACTTATCTGGGAAATGAAACATCTGTTTTTTGGGCCAACAGGAAACAAG 458
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/mol_type="genomic DNA"
/db_xref="taxon:4577"
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Gapop 10.0 , Gapext 1.0
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SUMMARIES
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BX757	BX75	BX75739	13	915	0	379.2	44
J4510	AJ451	AJ451	9	767	0	380.6	43
-In 967	BU63:	BU6332	13	825	40.3	382	42
716 AR064C0	BI30	BI30471	12	465	0	383.4	41
)42 BY734042	ВY73	BY734	13	661	40.7	385.8	40
	BG61:	BG61955	12	791	41.7	395	39
Ξ	BI08:	BI082	12	854	2	399.6	38
592 AV723592	AV723592 A	AV723592	9	484		421.2	37
Ξ.	CF72	CF724	14	690	4.	423.8	36
'n.	AU280:	AU28038	9	565	ū	429	35
~	BM74	BM7406	12	633	ū	430	34
91	CB45	CB4556	14	516	5	435	ω G
9857 7039h03.x	BF73	BF7	10	706	5	435.6	32
4284 hg57g10.x		AW5	10	599	٠,	442.4	31
7448 ik38b05.y		BQ41	13	623	7.	447.2	30
6284 603172673		BI45	12	853	œ	455.6	29
2240 UNL-P-FN-		BILE	12	796	œ	458.4	28
8221 AGENCOURT		CKL	14	833	9	468.2	27
4549 603356375		BI73	12	872	9	468.8	26
6421 602919530		BIL	12	828	0	474.6	25
9262 K-EST0129		BM8	12	607	0	475	24
5730 un71c09.y		AW4	10	777		489.4	23
9525 CITBI-E1-		AQ3(28	607	ν.	501	22
6170 AGENCOURT		EQ92	13	938	ω	506.2	21
0113 602782325		BG82	12	676	ω	507.8	20
9385 AGENCOURT		BQ91	13	974	5	522.8	19
di-		BQ4	13	755	57.2	542.6	18
7292 12B22045_		CB29	14	564	7.	546.2	17
6028		BIOE	12	915	ъ.	550.4	16
60230897	BF981	BF98215	10	1098	9	62	15
NISC npo	CB21!	CB21545	14	641	ω ·	600	14
60294192	BI22:	BI22353	12	787	u.	601	ü
60285567	BI090	BI09056	12	869	9	29	12
AGENCOUR	CA488	85	14	924	7.	43	11
0641 BX370641	BX370	7064	13	908	œ	45	10
Mus	AK032	3229	11	2247	٥.	9	9
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	JOURNAL COMMENT	TITLE	REFERENCE		ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION		DEFINITION	Locus	AL546472	RESULT 1
CONTACT: Genoscope Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France Bmail: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr Inbirary was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 7238.f For more information about this cluster, see http://www.genoscope.cns.fr/ cgi-bin/cluster.cgi?seq=CSODI030CE01QP1&cluster=7238.f. Contact: Feng Liang Email: fliang@lifetech.com URL:	Unpublished (2001) On Feb 15, 2001 this sequence version replaced gi:12879620.	Full-length cDNA libraries and normalization	1 (bases 1 to 1201) I.i. W. B. Gruber, C. Jessee, J. and Polaves, D.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo	Homo sapiens	Homo sapiens (human)	EST.	AL546472.2 GI:31268306	AL546472	clone CSODIO30YJ01 5-PRIME, mRNA sequence.	AL546472 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA	AL546472 1201 bp mRNA linear EST 31-MAY-2003		

Result

Score

Match Length DB ID

Query

864.8 691.8 683.6 674.2

91.2 73.0 72.1 71.1

1201 923 1077 1201

9 AL546472 13 BX331615 13 BX342662 9 AL571805

AL546472 AL546472 BX331615 BX331615 BX342662 BX342662 AL571805 AL571805

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://fulllength.invitrogen.com/ InVitroGen Corporation Faraday Avenue Genoscope sequence ID : CSODIO30CE01QP1. Location/Qualifiers
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                                                                                      AGTGGAGAACCTACTTATCTGGGAAATGAAACATCTGTTTTKGGGCAACAGGAAACAAG
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/mol_type="mRNA"
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95.4%;
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1 (Dases 1 to 923)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7238.f
more information about this cluster, see
http://www.genoscope.cns.fr/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cgi-bin/cluster.cgi?seq=CSODB009AB01QP1&cluster=7238.f. Contact Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InVitrogen Corporation 1600
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BP 191 91006 EVRY cedex - France
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Location/Qualifiers
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                                                                                                                                                          CGTCCAAAACCTGATCCTTATTGTCAAGCTAAGTATACTTTCTGTCCAACTGGCTCACCT
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GAATTTAAATATGGAĞACCTCCTGĞĞACACTTGAAAATTATGNATGNTGNCATTGGATTC
                                                                             ATCCCAGTTATGGAGGTGATGACATTGAAGTTTTTCGATTACAAGCCCCCAGTATGG
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/clone="CSODB009YC01"
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Pred. No. 1.2e-146;
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OG EURY COCKET TRAIN TREESGENOSCOPE.CDS. France TREESGENOSCOPE.CDS. France This sequence below This sequence below This sequence below This sequence below This sequence cons.fr/ Uster.cgi?seq=CSDDLO Later.cgi?seq=CSDDLO Later.cgi?seq=CSDDLO Later.cgi?seq=CSDDLO Later.cgi.seq=Cod This sequence This sequence	ACCUS METINITION MICCESSION MICCESSION	### AATGAAACAGGAATTTATTATGAGACATGGAATGTAAAAGCCAGCC	y 301 AACTGTACATTTCCCCATCCTCGACCTGAAATGGATGCCCCTTTCTGGTGTAATCAAGGC 360	У 241 AGAAGTACATTAACTGGCAAGAACTACACAATGGAATGG
661 AGTGGAGAACCTACTTATCTGGGAAACAACATCTGTTTTTTTT	Qy 361 GCTGCCTGCTTTTTTGAGGAAATTGATGATGATGATGAAGAAAATGGGAACATTAGTT 420	Qy 121 ATCCCAGTTATGGAGGGTGATGATGAAGTTTTTCGATTACAAGCCCCAGTATGG 180	Query Match 72.1%; Score 683.6; DB 13; Length 1077; Best Local Similarity 88.8%; Pred. No. 8.8e-145; Matches 700; Conservative 49; Mismatches 34; Indels 5; Gaps 2; Qy 1 CGGGTCTCGGGCATCCCCTCCCGGGCCACTGGCCGTGCCTACAAGCGCTTTGACTTC 60	primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

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Five prime end enriched, double-strand cDNA was with Not I and cloned into the Not I and EcoR V. the pCMVSPORT 6 vector. Library was normalized."
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7238.f
more information about this cluster, see
http://www.genoscope.cns.fr/
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1 (bases 1 to 1201)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization

Unpublished (2001)

On Feb 16, 2001 this sequence version replaced gi:12929467.
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                                                                                                                                                                                                                 GAAAAGGGGGCAGAGACATGGTTTGATTCCTACGACTGTTCCAAATTTGTGTTAAGGACC
ACAGGAAACAAGACTCTTGGTTTAGCCATAAAAAGATTTTATTACCCCCTTCAAACCACAT 768
                                                                    ATATTTCTTTACAGTGGAGAACCTACTTATCTGGGAAATGAAACATCTGTTTTTGGGCCA
                                                                                                                                   TTTAACAAGTTGGCTGAATTTGGAGCAGAGTTCAAGAACATAGAAACCAACTATACAAGA
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/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="Ist strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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/db_xref="taxon:9606"
/clone="CS0DI030YJ01"
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97.8%;
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Best Local :
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Tissue Procurement: ATCC
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NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health,
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http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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CAAGAACTACACAATGGAATGGTATGAACTTTTCCAACTTGGCAACTGTACATTTCCCCA
                    CAAGAACTACACAATGGAATGGTATGAACTTTTCCAACTTGGCAACTGTACATTTCCCCA 317
                                                                                               CCTCCTGGGACACTTGAAAATTATGCATGATGCCATTGGATTCAGAAGTACATTAACTGG
                                                                                                                                         TGATGATGACATTGAAGTTTTTCGATTACAAGCCCCAGTATGGGAATTTAAATATGGAGA
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                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                   /tissue_type="adenocarcinoma"
//lab_host="DH108 (phage resistant)"
/clone_lib="NH1 MGC 65"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo d'Average insert size 1.8 kb. Library constructed by Li Technologies. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                   clone="IMAGE:3854119"
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93.0%;
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Pred. No. 2.3e-142;
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AUS neonate cerebellum cDNA, RIKEN full-length enriched library, clone:A730075N08 product:similar to CEROID-LIPOPUSCINOSIS NEURONAL PROTEIN 5 (CLN5 PROTEIN) [Homo sapiens], full insert sequence.
                 Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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                                                                                                                                                               misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-Cho, Tsurumi-ku, Yokohama Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P. Fukuda, S., Furuno, M., Hanagaki, T., Haza, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Munazaki, A., Murata, M., Mishi, K., Nomura, K., Munazaki, R., Ohho, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M., and Hayashizaki, Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 2356)
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URL:http://fantom.gsc.riken.go.jp/.
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                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
/strain="C57BL/6J"
                                                                                                                                                                                      /tissue type="cerebellum"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="7 days neonate"
                                                                                                                                                                                                                                                                                                                           /db_xref="FANTOM_DB:A730075N08"
/db_xref="MGI:2408405"
                                                                              /note="similar to CEROID-LIPOFUSCINOSIS NEURONAL (CLN5 PROTEIN) [Homo sapiens] (SWISSPROT|075503, FASTY, 73.9%ID, 86.7%length, match=1041)"
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/clone="A730075N08"
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UI-H-FL1-bgb-i-07-0-UI.s1 NCI_CGAP_FL1 Homo sapiens
UI-H-FL1-bgb-i-07-0-UI 3', mRNA sequence.
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                                                                                                                                                                               TATGAAGAAATCCCTTTACCTATCAGAAACAAAACACTCTCTGGTTT
                                                                                                                                                                                                                                                                    TTGTTTTATAATTTTGAATATTGGTTTTTACCTATGAAATTCCCTTTTATTAAAATAACA 900
                                                                                                                                                                                                                                                                                                                       AGTGGAGAACCTTACTTATCTGGGAAATGAAACATCTGTTTTTTGGGCCCAACAGGAAACAAG
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                                                                                                                                                  TACGAAGAAACCCCGTTACCTACCCGACATACAACATTTACCGACTT 1076
                                                                                                                                                                                                                                       TTGTTTTATAACTTTGAGTATTGGTTTCTACCAATGAAACCCCCCCTTTGTCAAAATAACA
                                                                                                                                                                                                                                                                                                                                                               GAATTTCTGTTGAGTCTCTTGCAAATTTTTGATGCAGTGATTGTGCACAAACAGTTCTAT 840
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AACTGTACATTTCCCCCATCTCCGACCTGAAATGGATGCCCCTTTCTGGTGTAATCAAGGC 360
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0; Mismatches 172;
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Mammalia; Eutheria;
1 (bases 1 to 689)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Clone distribution information can be obtained from Dr. M. Bento Soares, bento-soares@uiowa.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seq primer: M13 FORWARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
Tissue Procurement: James Martin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BU621797.1
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                                                ATTAGTTCAAGTAGCAACTATATCAGGAAACATGTTCAACCAAATGGCAAAGTGGGTGAA
                                                                                                                                                                                                                                                                             TGGATTCAGAAGTACATTAACTGGCAAGAACTACACAATGGAATGGTATGAACTTTTCCA
                                                                                                          ACTTGGCAACTGTACATTTCCCCCATCTCCGACCTGAAATGGATGCCCCCTTTCTGGTGTAA
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                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /lab_host="DHIDB (Life Technologies)"
/clone lib="NGI CGAP FLI"
/clone lib="NGI CGAP FLI"
/note="Organ: Chondrosarcoma; Vector: pT7T3-Pac
(Pharmacia) with a modified polylinker; Site 1: EcoR I;
Site 2: Not I; NCI CGAP FLI is a normalized CDNA library
derived from a pool of mRNA obtained from 4 cell lines
from grade III chondrosarcoma tissues. The library was
constructed according to Bonaldo, Lennon and Soares,
Genome Research, 6:791-006, 1996. First strand CDNA
synthesis was primed with an oligo-dT primer containing a
Not I site. Double stranded cDNA was ligated to an EcoR I
adaptor, digested with Not I, and cloned directionally
into pT7T3-Pac vector. The oligonucleotide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(dT)18 tail. The sequence tag for this library is
GAGGTCGGTG. The cell lines were provided by Dr. James
Martin from the University of Iowa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sapiens (human)
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/db_xref="taxon:9606"
/clone="UI-H-FL1-bgb-i-07-0-UI"
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/lab_host="DH10B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tissue_type="Cell lines"
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Pred. No. 8.3e-142;
0; Mismatches 4;
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                      Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y., RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequence Cenome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus 10 days lactation, adult female mammary gland cDNA, RIKEN full-length enriched library, clone:D730033903 product:similar to CEROID-LIPOFUSCINOSIS NEURONAL PROTEIN 5 (CLN5 PROTEIN) [Homo sapiens], full insert sequence.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokoham Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Adachi J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P. Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Xouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Mishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagama, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Muramatu, M., and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Encyclopedia Project of Genome Exploration Research Group Genomic Sciences Center and Genome Science Laboratory in I Division of Experimental Animal Research in Riken contribu
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Analysis of the mouse transcriptome
of 60,770 full-length cDNAs
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Please visit our web site for further details.
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6 (bases 1 to 2433)
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URL:http://fantom.gsc.riken.go.jp/.
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HTC; CAP trapper.
Mus musculus (house mouse)
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Carninci, P. and High-efficiency
                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                        Mus musculus
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Hayashizaki,Y.
full-length c
                                                                                 Chordata;
Rodentia;
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                                                                              Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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26 (bases 1 to 2247)

27 (bases 1 to 2247)

28 Adachi J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Fukuda, S., Furuno, M., Hiramoto, K., Hiraoka, T., Hirozane, T., Hayashida, K., Hayatsu, N., Hiramoto, K., Konno, H., Kasukawa, T., Kasukawa, T., Kodh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saito, H., Sakai, C., Sakai, K., Sakazume, N., Okazaki, Y., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagama, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomazu, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y. Direct Submission

21 Submission

22 Submission

23 Submission

24 Submission

25 Submission

26 Submission

26 Submission

27 Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (16-UIL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-Cho, Tsurumi-ku, Yokoham Kanagawa 230-0045, Japan (E-mail:genome-res@gecriken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Group Phase I & II Team.
Analysis of the mouse transcriptome of 60,770 full-length cDNAs
                                                                                                                                                                                                                                                Please visit our web site for further URL:http://genome.gsc.riken.go.jp/URL:http://fantom.gsc.riken.go.jp/.
                                                                                                                                                                                                                                                                                                                                                        CDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Ri
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed t
                                                                                                                                                                                                                                                                                                                                    prepare mouse tissues.
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                                                 /db_xref="FANTOM_DB:6430516P20"
/db_xref="MGI:2395762"
                                                                                                                                     organism="Mus musculus"
/mol_type="mRNA"
                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                              /strain="C57BL/6J"
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Best Local Similarity
Matches 773; Conserv
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                                                                                                                                                                                                                                                                                                               AATGAAACAGGAATTTATTATGAGACATGGAATGTAAAAGCCCAGCCCAGAAAAGGGGGGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CGTCCAAAACCTGATCCTTATTGTCAAGCTAAGTATACTTTCTGTCCAACTGGCTCACCT 120
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                                                                       AGTGGAGAACCTACTTATCTGGGAAATGAAACATCTGTTTTTGGGCCCAACAGGAAACAAG
                                                                                                                                                        GCTGAATTTGGAGCAGAGTTCAAGAACATAGAAACCAACTATACAAGAATATTTCTTTAC
                                                                                                                                                                                                                                                                                                                                                                       GTCGTTGCAACCATATCCGGAAACACATTTAACAAAGTGGCCGAGTGGGTGAAGCAGGAC
                                                                                                                                                                                                                                                                                                                                                                                                     CAAGTAGCAACTATATCAGGAAACATGTTCAACCAAATGGCAAAGTGGGTTGAAACAGGAC
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ACTCTTGGTTTAGCCATAAAAAGATTTTATTACCCCCTTCAAACCACTTTGCCAACTAAA
                                        AGTGGAGAGCCTATTTACCTGGGAAATGAAACATCTATTTTTGGGCCCCAAAGGAAACAAG
                                                                                                                        GCTGAATTTGGAACAGAATTCAAGAAGATAGAAACAAACTATACGAAAATATTTCTTTAC
                                                                                                                                                                                                      CAGACGTGGTTCGAGTCCTACGACTGTTCGAATTTTGTCTTAAGGACATATAAGAAATTG
                                                                                                                                                                                                                                                                                     AATGAAACTGGGATTTATTATGAGACATGGACGGTCCGAGCCGGCCCAGGACAAGGGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                       AACTGTACATTTCCCCACCTCCGGCCTGACAAGAGCGCTCCCTTCTGGTGTAACCAAGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATCCCAGTTATGAAGGACAATGACGTCATCGAGGTCTTACGACTACAAGCCCCGATTTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTGGGCGCGTCCCCGACGTCTGGGCAACGCTGGCCGGTGCCATACAAGCACTTCTCTTTC
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/db_xref="d1:26328113"
/db_xref="d1:26328113"
/td=xref="d1:26328113"
/tznslation="LGLATILGASPTSGQRWPVPYKHFSFRPKTDPYCQAKYTFCPTG/bIPNKDNDVITEVLRLQAPIWEFKYSDLLGHFKLMHDAVGFRSTLTGKNYTTEWYELFQLGNCTFPHLRPDKSAPFWCNQGAACFFEGIDDKHWKENGTLSVVATISGNTFNKVAEWVKQDNETGIYYETWTVRAGPGQGAQTWFBSYDCSNFVLRTYKKLABFGTEFKKIET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="unnamed protein product; putative similar to CEROID-LIPOFUSCINOSIS NEURONAL PROTEIN 5 PROTEIN [Homo sapiens] (SWISSPROT|075503, evidence: PASTY, 73.9%ID, 86.7%length, match=1041)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /sex="male"
/tissue type="olfactory brain"
/clone_Tib="RIKEN full-length enriched mouse
/dev_stage="adult"
<1. _971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NYTKIFLYSGEPIYLGNETSIFGPKGNKTLALAIKKFYGPFRPYLSTKDFLMNFLKIF
DTVIIHRQFYLFYNFEYWFLPMKPPFVKITYEETPLPTRHTTFTDL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               codon_start=3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 668.6; DB 11;
Pred. No. 2.1e-141;
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334 GATGCCCCTTTCTGGTGTAATCAAGGCGCTGCCTGCCTTTTTTGAGGGAATTGATGATGTT 393	Ŋ
1 GTATGGTCTGGACTTTTCCACTTGGCAACTGGTACATTTTCCCCATCTCCGACCTG-AATG 59	Дb
274 GAATGGTATGAACTTTCCAACTTGGCAACTGTACATTTCCCCATCTCCGACCTGAAATG 333	γQ
y Match 68.1%; Score 645.4; DB 13; Length 908; Local Similarity 98.2%; Pred. No. 4.2e-136; hes 663; Conservative 0; Mismatches 11; Indels 1; Gaps 1;	Query Best L Matche
	ORIGIN
/note="1st strand cDNA was primed with a NotI-oligo(dT) /note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was primer. Five prime end enlohed, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."	
/cell_line="RAMOS CELL LINE" /clone_lib="Homo sapiens B CELLS (RAMOS CELL LINE) COT	
606" P03" LS (R	
Faraday Avenue Genoscope sequence ID : CSOBAG053ZH0: Location/Qualifiers 1908	FEATURES sou
ZH03 CS05016 1&cIuster=7238. ng@llfetech.com URL : InVitroGen Corporation 1600	
ary was constructed by Life Technologies, a division tropen. This sequence belongs to sequence cluster 723	
BP 191 91006 EVRY cedex - France BP 191 91006 EVRY cedex - France Email: secref@canoscope.cns.fr, Web : www.cenoscope.cns.fr	
Contact: Genoscope Genoscope - Centre National de c	COMMENT
Li, W.B., Grubes Full-length cDN	AUTHORS TITLE
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 908)	REFERENCE
NISM Homo sapiens Eukaryota: Metazoa: Chordata: Craniata:	ORGANISM
EST. Homo sapiens (human)	KEYWORDS SOURCE
ON BX370641	ACCESSION VERSION
BX370641 Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED Homo sapiens cDNA clone CS0DL004YP03 5-PRIME, mRNA sequence.	DEFINITION
) BX370641 908 bp mRNA linear	RESULT 10 BX370641 LOCUS
921 TACGAAGAAACCCCGTTACCTACCCGACATACAACATTTACCGACTT 967	DЬ
901 TATGAAGAAATCCCTTTACCTATCAGAAACAAAACATCTCTCTGGTTT 947	Qy
861 TIGITITATAACITIGAGTATIGGTITCTACCAATGAAACCCCCCTTIGTCAAAATAACA 920	Дb
841 TIGTTTTATAATTTTGAATATTGGTTTTTACCTATGAAATTCCCCTTTTATTAAAATAACA 900	ρ
GATTTTCTGATGAATTTCTTGAAAATTTTTGATACAGTGATTATACACAGACAG	Db
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741 ACTCTTGCTTTGGCCATAAAAAATTTTATGGCCCCTTCAGACCGTATTTGTCAACCAAA 800	dd

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                                                                                                 Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Kristi A. Egland, Ira Pastan
cDNA Library Preparation: Invitrogen Corp
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llni.gov
plate: LLAM14279 row: j column: 21
                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 924)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
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CA488543.1 GI:24950702
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                                                                                    e: LLAM14279 row: j column: quality sequence stop: 637.
 /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6720309"
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869 602855673F1 NIH_MGC_10 Homo smRNA sequence._
BI090566
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                                                                                                                                                                                                                                                             GAGACATGGTTTGATTCCTACGACTGTTCCAAATTTGTGTTAAGGACCTTTAACAAGTTG
                                                                                                                ACAGTGGGAGAAACCTTACT
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765 660 600

645

705

sapiens

mRNA cDNA clone

linear EST 20-J Cone IMAGE:4996891

EST 20-JUN-2001 3:4996891 5',

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Query Match
Best Local Similarity
AATGAAACAGGAATTTATTATGAGACATGGAATGTAAAAGCCCAGCCCAGAAAAGGGGGCCA
                                                                                             CAAGTAGCAACTATATCAGGAAACATGTTCAACCAAATGGCAAAGTGGGTGAAACAGGAC
                                                                                                                                                                                                GAATTTAAATATGGAGACCTCCTGGGACACTTGAAAATTATGCATGATGCCATTGGATTC
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                                                                CAAGTAGCAACTATCAGGAAACATGTTCAACCAAATGGCAAAGTGGGTGAAACAGGAC
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Subtracted with brain, liver, lung, kidney and muscle.
Directionally cloned. Priming method: oligo-dT. Average
insert size: 1800 bp. Library amplification: 26,000 fold.
Kristi A. Egland, James J. Vincent, Robert Strausberg,
Bungkook Lee & Ira Pastan: Discovery of new breast
cancer genes encoding membrane and secreted proteins.
Manuscript submitted."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /cell line="ZR-75-1, MCF7, SK-BR-3, MDA-MB-231, hTERT-HME1, LNCap"
/lab host="EMCH10B"
/clone_lib="MAPcL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67.8%;
96.6%;
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Pred. No. 1.3e-135;
0; Mismatches 23;
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Best Local Similarity 96.8
Matches 706; Conservative
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NIH-WC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection
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Location/Qualifiers
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Tissue Procurement: ATCC
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http://image.llnl.gov
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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 GAATTTAAATATGGAGACCTCCTGGGACACTTGAAAATTATGCATGATGCCATTGGATTC
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Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.5 kb. Library prepared by Life
Technologies."
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/lab_host="DH10B"
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CGTCCAAAACCTGATCCTTATTGTCAAGCTAAGTATACTTTCTGTCCAACTGGCTCACCT
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cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: Incyte Genomics, Inc. DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information found through the I.M.A.G.B. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
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Location/Qualifiers
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Site_2: Sall; Cloned unidizectionally. Primer: Oligo dT.
Average insert size 1.4 kb. Library prepared by Life
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                                                                                                                                                                                                                                                                                                                                                                         tissue_type="cervical carcinoma cell
lab_host="DH10B"
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Pred. No. 5.1e-126;
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NISC np06c07.y1 NICHD HS Ut1
5', mRNA sequence.
CB215456
CB215456 GI:28263648
                                                                                                                        DNA Sequencing by: National Institutes of Health Sequencing Center (NISC)
Clone distribution: NCI-CGAP clone distribution
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL

cDNA Library Arrayed Institutes of Health Intram
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
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1 (bases 1 to 641)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
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                                                                         info@image.llnl.gov
Plate: LLAM13163 ro
                                                                                                            found through the I.M.A.G.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAGACATGGTTTGATTCCTACGACTGTTCCAAATTTGTGTT-AAGGACCTTTAACAAGTT 599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTACACTGG 783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGCTGA-ATTTGGAGCAGAGTTCAAGAACATA-GAAACCAACTATACAAG-AATATTTCT 656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAAGTAGCAACTATATCAGGAAACATGTTCAACCAAATGGCAAAGTGGGTGAAACAGGAC 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTACAGTGG 665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGCTGACATTTGGAGCAGAGTTCAAGAACATACGAAACCAACTATACAAGAAATACTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAGACATGGTCTGATT
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                                                        primer: M13RP1 reverse primer
   /organism="Homo sapiens"
                                        Location/Qualifiers
                                                                       row: E column:
                                                                                                                                                                                                                                                                                                                                  Chordata; Craniata; Vertebrata; Euteleostomi Primates; Catarrhini; Hominidae; Homo.
                                                                                                             Consortium/LLNL
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                       602308976F1 NIH_MGC_88 Homo sapiens
                                    Homo sapiens
                                                                                       BF982158.1
                                                                                                                        mRNA sequence.
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                                                                                                                                                                                                                                                                  GAGACATGGTTTGATTCCTACGACTGTTCCAAATTTGTGTTAAGGACCTTTAACAAGTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="normal endometrium, late proliferative phase, Cycle day 13"
/lab_host="DH10B (T1-resistant)"
/clone_lib="NICHD HS_Utl"
/clone_lib="NICHD HS_Utl"
/note="Organ: uterus; Vector: pCMV-SPORT6.1.ccdb (ResGen, Invitrogen Corporation); Site_1: NotI; Site_2: EcoRV; Cloned unidirectionally from microquantity amounts of mRNA from normal endometrial tissue (late proliferative phase, cycle day 13). Average insert size 1.9 kb. Library constructed by ResGen (Invitrogen Corporation)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5937013"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /sex="female"
                                                      (human)
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cDNA clone IMAGE:4400298
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541 GAGACATGGTTTGATTCCTACGACTGTTCCAAATTTGTGTTAAGGACCTTTAACAAGTTG
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can ?
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10105 row: 9 column: 19
High quality sequence stop: 693.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 1098)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                 AATGAAACAGGAATTTATTCTGAGACCTGGCCTGTCACAGCCAG-CCAGAACACGGGGCA
                                                                                                                                                                                         AATGAAACAGGAATTTATTATGAGACATGGAATGTAAAAGCCAAGCCCAGAAAAGGGGGCA 540
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/clone="MAGE: 4400298"
/tissue_type="duodenal adenocarcinoma, cell line"
/lab host="PHIOB (phage-resistant)"
/clone_lib="NIH_MGC_88"
/note="Organ: small_intestine; Vector: pCMV-SPORT6;
Site_1: Not1; Site_2: Sal1; Cloned unidirectionally;
oligo-dT primed. Average insert size 1.767 kb. Library
enriched for full-length clones and constructed by Life
Technologies. Note: this is a NIH_MGC Library."
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/mol_type="mRNA"
/db_xref="taxon:9606"
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Pred. No. 2.9e-117;
0; Mismatches 76;
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CCCCTCGGTTCTTCCTCAAAGAGAATTT
                                                     GGGGGAAACTAGTCTTTGGCGCGATGTCACA---
                                                                                                     GCTGAATTTGGAGCAAGATCCAGAACCTGA----ACCATATCCCGAATATTCCTCACC
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                          ACTCTTGGTTTAGCCATAAAAAGATTTT 748
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CURRENT APPLICATION NUMBER: US/10/653,595
CURRENT FILING DATE: 199-09-13
PRIOR APPLICATION NUMBER: US/97945
PRIOR FILING DATE: 1999-09-17
PRIOR APPLICATION NUMBER: PCT/US99/05804
PRIOR APPLICATION NUMBER: PCT/US99/05804
PRIOR FILING DATE: 1998-03-19
PRIOR PELLING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/078,576
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/078,573
PRIOR APPLICATION NUMBER: 60/078,573
PRIOR PILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/078,574
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/078,579
PRIOR APPLICATION NUMBER: 60/078,579
PRIOR APPLICATION NUMBER: 60/080,314
PRIOR PRIOR PILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080,314
PRIOR PILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080,314
PRIOR PILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080,312
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PRIOR APPLICATION NUMBER: 60/080,312
PRIOR APPLICATION NUMBER: 60/078,578
PRIOR APPLICATION NUMBER: 60/078,578
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PRIOR APPLICATION NUMBER: 60/078,578
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US-10-653-595-26
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                                                                                                                            SOFTWARE: Pa
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Publication No. US20040048304A1
                       NAME/KEY: SITE
                                                                                                                                            Remaining Prior Application data removed NUMBER OF SEQ ID NOS: 470 SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Ruben et. al.
TITLE OF INVENTION: 95 Human secreted proteins
FILE REFERENCE: PZ027P1C1
                                                                                            LENGTH: 17
TYPE: DNA
LOCATION: (1520)
OTHER INFORMATION: n equals a,t,g,
FEATURE:
                                                                           ORGANISM: Homo sapiens
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; LOCATION: (1741)
; OTHER INFORMATION:
US-10-653-595-26
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Best Local Similarity
Matches 1067; Conser
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OTHER INFORMATION:
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OTHER INFORMATION:
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LOCATION: (1689)
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                             GCAGAGACATGGTTTGATTCCTACGACTGTTCCAAATTTTGTGTTTAAGGACCTTTAACAAG
                                                                                          GACAATGAAACAGGAATTTATTATGAGACATGGAATGTAAAAGGCCAGCCCAGAAAAAGGGG
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                                                                      GTTCAAGTAGCAACTATATCAGGAAACATGTTCAACCAAATGGCAAAGTGGGTGAAACAG
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Pred. No. 3.2e
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RESULT 4
US-09-397-945-26
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      FEATURE:

RAME/KEY: SITE
LOCATION: (1520)
OTHER INFORMATION: r
NAME/KEY: SITE
LOCATION: (1557)
                                                                                                                                              SOFTWARE: PatentIn
SEQ ID NO 26
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PRIOR FILING DATE: 1998-04-01
NUMBER OF SEQ ID NOS: 470
SOFTWARE: Patentin Ver. 2.0
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PRIOR FILING DATE: 1998-03-19
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PRIOR FILING DATE: 1999-03-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Human Genome Sciences, Inc. et al. TITLE OF INVENTION: 95 Human secreted proteins
                                                                                                LENGTH: 1751
TYPE: DNA
ORGANISM: Homo sapiens
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OR FILING DATE: 1998-03-19

DR APPLICATION NUMBER: 60/078,577

DR FILING DATE: 1998-03-19

DR APPLICATION NUMBER: 60/078,563

DR FILING DATE: 1998-03-19
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FILING DATE: 1998-03-19
APPLICATION NUMBER: 60/078,579
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FILING DATE: 1998-03-19
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Best Local Similarity
Matches 1067; Conserv
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NAME/KEY: SITE
LOCATION: (1729)
OTHER INFORMATION: I
NAME/KEY: SITE
LOCATION: (1735)
OTHER INFORMATION: I
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LOCATION: (1741)
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Pred. No. 3.2e-278;
2; Mismatches 2;
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COTHER INFORMATION: n is any nucleotide US-09-122-383-13
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LENGTH: 1038
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SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Sheppard, Paul O.
APPLICANT: Gilbertson, Debra G.
TITLE OF INVENTION: SECRETED PROTEINS ENCODED
TITLE OF INVENTION: CHROMOSOME 13
FILE REFERENCE: 97-38
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Pred. No. 1.7e-198;
2; Mismatches 165;
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                                 APPLICANT: Schepard, Paul O.
APPLICANT: Gilbertson, Debra G.
FITLE OF INVENTION: SECRETED PROTEINS ENCODED
FITLE OF INVENTION: CHROMOSOME 13
FILE REFERENCE: 97-38C1
CURRENT FILING DATE: 2002-03-26
PRIOR APPLICATION NUMBER: US 09/122,383
PRIOR FILING DATE: 1998-07-24
PRIOR APPLICATION NUMBER: US 60/053,613
PRIOR TILING DATE: 1997-07-24
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13
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  TYPE: DNA
                            LENGTH: 1038
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TAYCCNTTYAARCCNCAYYTNCCNACNAARGARTTYYTNYTNWSNYTNYTNCARATHTTY
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Pred. No. 1.7e-198;
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CURRENT FILLING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILLING DATE: 2000-02-04
PRIOR FILLING DATE: 2000-02-04
PRIOR FILLING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILLING DATE: 2000-08-03
PRIOR FILLING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILLING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
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US-09-864-761-22592
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SOFTWARE: Annomax Sequence
SEQ ID NO 22592
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                                                                                  LENGTH: 494
TYPE: DNA
ORGANISM: Homo s
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PRIOR FILING DATE: 2001-01
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TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
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APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K
APPLICANT: Chen, Wensheng
FEATURE:
OTHER INFORMATION: MAP TO AC001226.1
OTHER INFORMATION: EXPRESSED IN PLACENTA,
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                                                                                                                                                                                                                                                                                                                                                   OR APPLICATION NUMBER: PCT/US01/00662
OR FILING DATE: 2001-01-30
OR APPLICATION UNMBER: PCT/US01/00661
OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: PCT/US01/00670
OR APPLICATION NUMBER: PCT/US01/00670
OR PETLING DATE: 2001-01-30
OR APPLICATION NUMBER: US 60/234,687
OR APPLICATION NUMBER: US 60/234,687
OR FILING DATE: 2000-09-21
                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 09/608,408
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Hanzel, David K.
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                                                                                                 Merberg, David
Treacy, Maurice
Spaulding, Vikki
TITLE OF INVENTION: SECRETED,
NUMBER OF SEQUENCES: 1519
                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute,
STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                   1074
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INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 5.8
INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 5.8
INFORMATION: EXPRESSED IN LING, SIGNAL = 3.6
INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.9
INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.9
INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 5.3
INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 5.3
INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 5.3
INFORMATION: SWISSPROT HIT: 075503, EVALUE 0.00e+00
INFORMATION: EST_HUMAN HIT: H01255.1, EVALUE 0.00e+00
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Similarity 100.0%;
             CITY: Cambridge
STATE: Massachusetts
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COUNTRY: U.S.A
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LaVallie, Edward
Racie, Lisa
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Pred. No.
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GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David K.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                        Sequence 5832, Application US/09864761 Patent No. US20020048763A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 402; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEPAX: (617) 876-5851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 825:
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ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US/10/040,739
FILING DATE: 07-Jan-2002
CLASSIFICATION: <Unknown>
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MEDIUM TYPE: Floppy Disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 506 base pairs
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                                                                                                                                                                                                                       Best Local Sin Matches 382;
                                                                                                                                                                                                                                                            Query Match
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PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
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CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: MAP TO ACCO1226.1
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 4.5
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 6.3
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 5
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.6
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.6
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.9
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 4.2
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 4.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
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APPLICATION NUMBER: PCT/US01/00665
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APPLICATION NUMBER: PCT/US01/00661
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APPLICATION NUMBER: PCT/US01/00668
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                                                                                                                                                                                                                                          Similarity
                     TGATTCCTACGACTGTTCCAAATTTGTGTTAAAGGACCTTTAACAAGTTGGCTGAATTTGG
TGATTCCTACGACTGTTCCAAATTTGTGTTAAGGACCTTTAACAAGTTGGCTGAATTTGG
                                                                       AATTTATTATGAGACATGGAATGTAAAAGCCAGCCCAGAAAAGGGGGGCAGAGACATGGTT
                                                                                                        AATTTATTATGAGACATGGAATGTAAAAGCCAGCCCAGAAAAAGGGGGGCAGAGACATGGTT
                                                                                                                                              TAAACTAGGAAACATGTTCAACCAAATGGCAAAGTGGGTGAAACAGGACAATGAAACAGG
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99.2%;
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Pred. No. 2.1e-92;
0; Mismatches 3
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US-10-264-049-1859
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SOFTWARE: PatentIn Ver. 3.:
SEQ ID NO 1859
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/264,049
CURRENT FILING DATE: 2002-10-04
PRIOR APPLICATION NUMBER: PCT/US01/18569
PRIOR FILING DATE: 2001-06-07
PRIOR APPLICATION NUMBER: US 60/209,467
PRIOR FILING DATE: 2000-06-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Birse et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PA133P1
                                                                                                                                                                                                                                                                                                                       FEATURE: Feature NAME/KEY: misc feature (295) (295) (295)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc feature LOCATION: (2). (2) OTHER INFORMATION: n equals
                                                                                                                                                                                   NAME/KEY: misc_feature
LOCATION: (323)..(324)
OTHER INFORMATION: n e
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NAME/KEY: misc_feature
LOCATION: (313)...(313)
OTHER INFORMATION: n equals
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NAME/KEY: misc_feature
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LOCATION: (175)..(175)
OTHER INFORMATION: n equals
FEATURE: misc feature NAME/KEY: misc feature LOCATION: (440)..(440) OTHER INFORMATION: n ec
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OTHER INFORMATION: n equals
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                                                           LOCATION: (395)..(395)
OTHER INFORMATION: n equals
                                                                          NAME/KEY: misc feature LOCATION: (395)..(395)
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LOCATION: (331)..(331)
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US-09-867-701-2579
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                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/867,701
CURRENT FILING DATE: 2001-05-29
NUMBER OF SEQ ID NOS: 10912
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2579
LENGTH: 351
TYPE: DNA
ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2579, Application US/09867701 Patent No. US20020132237A1 GENERAL INFORMATION:
                                                                                                       Matches
                                                                                                                    Query Match
Best Local Similarity
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                            APPLICANT: Aglate, Paul A.
APPLICANT: Jones, Robert
APPLICANT: Harlocker, Susan L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.497
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LOCATION: (483)...(483)
OTHER INFORMATION: n equals a,t,g,
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LOCATION: (478)...(478)
OTHER INFORMATION: n equals
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LOCATION: (464)..(464)
OTHER INFORMATION: n equals
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OTHER INFORMATION: n equals
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LOCATION: (458)..(458)
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438 ACTGTACATTTCCCCATCTCCGACCTGAAATGGATGCCCCTTTCTGGTGTAATCAAGGCG 497
                                                                 378 GAAGTACATTAACTGGCAAGAACTACACAATGGAATGGTATGAACTTTTCCAACTTGGCA 437
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                                  GAAGTACATTAACTGGCAAGAACTACACAATGGAATGGTATGAACTTTTCCAACTTGGCA
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Pred. No. 7.2e-43;
0; Mismatches 43
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Pred. No. 2e-61;
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SOPTWARE: Patentin version 3, SEQ ID NO 1363; ELENGTH: 473; TYPE: DNA CORGANISM: Homo sapiens US-09-954-456-1363
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US-09-954-456-1363/c
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APPLICANT: Young, Paul
APPLICANT: Young, Paul
TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Cance
TITLE OF INVENTION: Sets
                                                                                                                                                                                                                                                Matches
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                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
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CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: US/60/233,617
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: US/60/234,052
PRIOR FILING DATE: 2000-09-20
PRIOR PILING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: US/60/234,923
PRIOR FILING DATE: 2000-09-25
PRIOR FILING DATE: 2000-09-25
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PRIOR FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/60/235,863 FILING DATE: 2000-09-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/60/235,840 FILING DATE: 2000-09-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/60/235,638 FILING DATE: 2000-09-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/60/235,637 FILING DATE: 2000-09-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/60/235,720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/60/235,711
                                      1072
                                                                                                                       1012 GAAATTCCCTTTTATTAAAATAACATATGAAGAAATCCCTTTACCTATCAGAAACAAAAC 1071
                                                                                                                                                                  473
353
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                                    ACTCTCTGGTTTA 1084
                                                                                                                                                                  <u>ÁGTGÁTTGTGCACAAACAGTTCTATTTGTTTTATAATTTTGAATATTTGGTTTTTACCTAT</u>
                                                                                                                                                                                        AGTGATTGTGCACAAACAGTTCTATTTGTTTTTATAATTTTGAATATTTGGTTTTTTACCTAT 1011
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                                                                                GAAATTCCCTTTTATTAAAATAACATATGAAGAAATCCCTTTACCTATCAGAAACAAAAC
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ACTCTCTGGTTTA 341
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                                                                                                                                                                                                                                                                 12.3%; Score 133; DB 9; 1 100.0%; Pred. No. 2.3e-25;
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RESULT

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PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 5232
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                                                                                                                                                                                                                                                          ; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-5232
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US-09-938-842A-5232
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-908-975-10339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
TITLE OF INVENTION: SCRIP1300-3
FILE REFERENCE: SCRIP1300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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Best Local
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APPLICANT: MINTZ, LIAU
APPLICANT: FAIGLER, Simchon
TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND
TITLE OF INVENTION: THAT POPULATE A TRANSCRIPTOME
FILE REFERENCE: 36688-0005
CURRENT APPLICATION NUMBER: US/09/908,975
CURRENT FILING DATE: 2001-07-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 32337
SOFTWARE: PatentIn version 3.0
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PRIOR APPLICATION NUMBER: US 60/287,724
PRIOR FILING DATE: 2001-05-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 60/221,607
PRIOR FILING DATE: 2000-07-28
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                                                                                                                                                                         121;
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Similarity 100.0%;
60; Conservative (
                                                                                                                                                                                                Similarity
AAACTGCTTCTTCATGTGCCTACCAAAAAAAAAAAACTGCTTCTTCATGTGGCTTCTAAGT 240
                                     AAATGAAACATCTGTTTTTGGGCCAACAGGAAACAAGACTCTTGGTTTAGCCATAAAAAG 879
                                                                                 GAATATAGATTTCATCCCTGTGATTATGTTTATATATGGAAATTGAGTTTTACAAGAGTG
                                                                                                                             GAACATAGAAACCAACTATACAAGAATATTTCTTTACAGTGGAGAACCTACTTATCTGGG 819
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49.0%;
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                                                                                                                                                                    Score 45.4; DB 9; Length 1
Pred. No. 0.33;
0; Mismatches 126; Indels
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hes 0;
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APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
APPLICANT: Zhu, Tong
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRA
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
PRIOR FILING DATE: 2001-06-22
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US-09-938-842A-5232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 5232
                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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APPLICANT: Kreps, Joel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
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nes 121; Conserv
                                         1000 GTTTTTA 1006
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361
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                                                                                                                                                                                                                                                                                                                                                       121 GAATATAGATTTCATCCCTGTGATTATGTTTATATATGGGAAATTGAGTTTTACAAGAGTG
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                                                                                                                                                                          GTTTAATTACGCCTTCAGCAACATGTAGAGATCTTGAGAAATTGACATGAGTCTCTAGAG 300
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                                                                                                                              AATTITTGATGCAGTGATTGTGCACAAACAGTTCTATTTGTTTTTATAATTTTGAATATTG 999
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GCCTGTA 367
                                                                                  AATGTTGAAAGCTGTGGTCGTTGACCAAGAAGATTCTTACTATTTGACTCTATTTGATAG
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Pred. No. 0.33;
0; Mismatches 126;
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Search completed: April 22, 2004, 05:09:05
Job time : 848.604 secs

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Result
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Maximum I
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Maximum Match 100%
Listing first 45 summaries
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          DB seq length: 0
DB seq length: 2000000000
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      d. No. is the number of results predicted by chance to have a
re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Issued_Patents NA:*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfīles1.seq:*
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Gapop 10.0 , Gapext 1.0
  4.7 7218
3.8 640681
3.7 2772
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3.6 21721
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Sequence 14, Appli
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a a

Query Match

4.7%;

Score

50.6;

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Length 7218;

Stephen A. NUMBER: 29 KET NUMBER: ON INFORMAT 703)836-930 3)683-4109 9 EQ ID NO: TERIFICS: base pairs c acid single near E: E: F1s	CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/232,463 FILING DATE: CLASSIFICATION: 435 PRIOR APPLICATION DATA: APPLICATION NUMBER: US/07/935,313 FILING DATE: APPLICATION NUMBER: EP 91 114 300.6 FILING DATE: 26-AUG-1991 ATTOORNEY ARRYT INSPERANTION.	ADDRESS: ROLey & Lardner O Diagonal Road, Suite 500 ondria A A O299 BLE FORM: Floppy disk Floppy disk BM PC compatible STEM: PC-DOS/MS-DOS atentIn Release #1.0, Version #1.	RESULT 1 US-09-232-463-14/c ; Sequence 14, Application US/08232463 ; Patent No. 5670367 ; Patent No. 5670367 ; APPLICANT: DORNER, F. APPLICANT: SCHEIFLINGER, F. APPLICANT: RAIKNER, F. F. TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS ; NUMBER OF SEQUENCES: 52	36 3.3 13086 4 US-08-956-171E-16 36 3.3 43280 2 US-08-804-227C-1 35.6 3.3 363 4 US-09-601-198-169 35.4 3.3 447 4 US-09-611-976-281 35.4 3.3 1164 1 US-08-416-478A-51 35.4 3.3 1164 2 US-08-474-988B-5 35.4 3.3 1164 2 US-08-394-442B-5 35.4 3.3 11654 4 US-09-620-312D-58	.4 4411529 3 US-09-10: .4 1830121 4 US-09-64: .4 1830121 4 US-09-64: 1 1767 4 US-09-016: .4 1664976 4 US-08-91: .3 9347 4 US-10-204: .3 364 3 US-08-897 .3 364 4 US-09-621 .3 6757 4 US-09-623
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SEQ ID NO 1
LENGTH: 640681
TYPE: DNA
ORGANISM: Buchnera sp.
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Matches
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Best Local Similarity
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APPLICANT: WATANABB, HIDEMI
APPLICANT: HATTORI, MASAHIRA
APPLICANT: SAKAKI, YOSHIYUKI
TITLE OF INVENTION: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS
                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: 081356/0159
CURRENT APPLICATION NUMBER: US/09/790,988
CURRENT FILING DATE: 2001-02-23
                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 7
                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: JP2000-107160 PRIOR FILING DATE: 2000-04-07
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23; Conserv
ATTTTATTACCCCTTCAAACCACATTTGCCAACTAAAGAATTTCTGTTGAGTCTCTTGCA 939
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                                                                                     AAACATCTGTTTTTGGGCCAACAGGAAACAAGACTCTTGGTTTAGCCAT-----AAAAAG
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                                                                                                                                                                                          Conservative
                                                                                                                                                                                                         3.8%;
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Pred. No. 3.4;
0; Mismatches 108; Indels 5;
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US-08-500-857A-7
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US-08-500-857A-7
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Best Local S
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APPLICANT: OHATA, SHOZO
APPLICANT: USAMI, STORU
APPLICANT: BURNELL, JAMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 103-205-8050 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MURCHY JR, GERALD M
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 760-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: BURNELL, JAMES N
TITLE OF INVENTION: POLYPEE
TITLE OF INVENTION: ORTHOPH
TITLE OF INVENTION: AND REC
TITLE OF INVENTION: THE DNA
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: other nucleic FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/500,85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: BIRCH, STEWART, KOLASCH AND
STREET: 8110 GATE HOUSE ROAD SUITE 500
CITY: FALLS CHURCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: U.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH:
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                                                                                                                                                                                       518 CAAAAAGTTGAAAAGGGAGTTAAATTAGATACTGAATTAGATGCTAATGATATGAAAGA 577
                                                                                                                                                                                                                          586 CAACCAAATGGCAAAGTGGGTGAAACAGGACAATGAAACAGGAATTTATTATGAGACATG 645
                                     638 TCCÁTATGCTCAÁTTAGAATTTGCCÁTTTGTGCTGTÁTTCAGÁTCATGGATGGGAAAGAG
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AGAAACCAACTATACAAGAATATTTCTTTACAGTGGAGAACCTACTTATCTGGGAAATGA 825
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ilarity 46.3%;
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ORTHOPHOSPHATE DIKINASE ACTIVITY, DNA ENCODING THE SAME
AND RECOMBINANT VECTOR AND TRANSFORMED PLANTS CONTAINING
THE DNA
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Pred. No. 0.2;
0; Mismatches 154;
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EAST
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Patent No. 5891855
                          Sequence 1, Application US/09211290
Patent NO. 6071885
GENERAL INFORMATION:
APPLICANT: Florkiewicz, Robert Z.
APPLICANT: Florkiewicz, Robert Z.
APPLICANT: Florkiewicz, Robert Z.
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UNMER: US/08/599,895
FILING DATE: 31-JAN-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: No. 5891855tenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
REGISTRATION NUMBER: 39,317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 76
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Florkiewicz, Robert Z.
TITLE OF INVENTION: INHIBITORS OF LEADERLESS PROTEIN EXPORT
NUMBER OF SEQUENCES: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
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TYPE: single
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SEED and BERRY LLP
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Patent No. 6107283
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
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NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/211,290
FILING DATE: 12-DEC-1998
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CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                               FILING DATE: CLASSIFICATION:
                                                                                                                                                                  APPLICATION NUMBER:
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682-6031
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Pred. No. 0.37
0; Mismatches
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ATTORNEY/AGENT INFORMATION:

NAME: Maki, David J. REGISTRATION NUMBER: 31,392

200124.401D1

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RESULT 7
US-09-466-036A-1
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GENERAL INFORMATION:
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                                                                                                          TELEFAX: (206) 682-
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
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                                                                                                                                                               APPLICATION NUMBER: US 09/211,290
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 200124.401D1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                     CLASSIFICATION: <Unknown> PRIOR APPLICATION DATA:
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                                                                                              SEQUENCE CHARACTERISTICS:
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                               LENGTH: 3877 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/09/466,036A FILING DATE: 17-Dec-2001
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                                                                                                                                                 TELEPHONE:
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DESCRIPTION: SEQ ID NO: 1:
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Pred. No. 0.37;
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Matches
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Matches
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Best Local Similarity
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APPLICANT: HESSE,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Wong, King L.
REGISTRATION NUMBER: 37,500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
COMPUTER: OF COMPATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: RECOMBINANT PROTEINASE FROM CLOSTRIDIUM
TITLE OF INVENTION: HISTOLYTICUM AND ITS USE FOR ISOLATING CELLS AND GROUPS OF CELL
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nikaido, Marmelstein, Murray & Oram LLP
STREET: 655 15th St., N.W., Suite 330 - G St. Lobby
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 2428 base pair
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
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Pred. No. 0.37;
                                Score 39.6; DB Pred. No. 0.37;
   Mismatches
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RESULT 10
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US-09-621-976-2813/c
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US-09-621-976-2813
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APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
                                                            Sequence 71, Application US/10204708 Patent No. 6677731
GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patent.pm
SEQ ID NO 2813
LENGTH: 832
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Patent No. 6639063
GENERAL INFORMATION:
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Best Local :
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NAME/KEY: CDS
LOCATION: 235.
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CURRENT FILING DATE: 2000-07-21
                   APPLICANT: PIEPENBROCK, Christian APPLICANT: BERLIN, Kurt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 19335
TITLE OF INVENTION: Diagnosis of Diseases Associated with
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GSTYWTMKCTCATWCYWYWKYWKRMWSKTCWSGSRGGYMTSYTSTRSYSMYWASWMYTMC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WKRMMSTRWYCYMCWKCCMYRGRRCAWYTMARGRMWSYAWGKWKSMRSAMSMCTRMYYKK 248
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Pred. No. 0.25;
74; Mismatches 142;
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    DNA Replication
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RESULT 11
US-09-269-939A-41/c
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; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-204-708-71
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CURRENT FILING DATE: 2003-05-06
PRIOR APPLICATION NUMBER: PCT/EP01/03971
PRIOR FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: DE 10019058.8
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
PRIOR PILING DATE: 2000-04-07
PRIOR PILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
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                                                                                                                                                                    SOFTWARE:
SEQ ID NO 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 41, Application US/09269939A Patent No. 6635431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 3.6%;
Best Local Similarity 48.2%;
Matches 110; Conservative
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SEQ ID NO 71
                                                                                                                                                                                                    APPLICANT: Bougueleret, Lydie
APPLICANT: Yen-Pottn, Frances
TITLE OF INVENTION: LSR Receptor, Its Activity, Its Cloning and Its Application To
TITLE OF INVENTION: The Diagnosis Prevention And/or Treatment of Obesity and
TITLE OF INVENTION: Related Risks or Complications
FILE REFERENCE: GENSET .035APC
CURRENT APPLICATION NUMBER: US/09/269,939A
CURRENT APPLICATION NUMBER: FR 97/10088
PRIOR APPLICATION NUMBER: FR 98/10088
PRIOR APPLICATION NUMBER: FR 98/05032
PRIOR FILING DATE: 1998-04-22
NUMBER OF SEQ ID NOS: 41
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APPLICANT:
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LOCATION:
NAME/KEY:
LOCATION:
                                                                                                          ORGANISM: Homo sapiens
                                                                                                                                TYPE: DNA
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TYPE: DNA
ORGANISM: Artificial Sequence
                                                                 FEATURE:
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Pred. No. 1;
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NAME/KEY: Misc_Feature
LOCATION: 11478
OTHER INFORMATION: diverging mucleotide,
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OTHER INFORMATION: diverging nucleotide, G in NAMS/KEY: Misc_Feature
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LOCATION: B604
OTHER INFORMATION: diverging
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LOCATION: 1229
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OTHER INFORMATION: diverging insertion, GAATGAAA in ref genbank:AD000684
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OTHER INFORMATION: diverging nucleotide, G
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LOCATION: 7337
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OTHER INFORMATION: diverging deletion,
                                                                                                                                                                                                                                                                                NAME/KEY: Misc_Feature LOCATION: 11577
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LOCATION: 9878
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                                                                                                   OTHER INFORMATION: diverging nucleotide,
                                                                                                                                                                                                        LOCATION: 1177\overline{9}
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                                                                                                                                                       OTHER INFORMATION: diverging deletion,
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INFORMATION: diverging nucleotide,
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                                                                                      Feature
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                                                  diverging nucleotide,
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US-09-269-939A-19/c
; Sequence 19, Application
; Patent No. 6635431
; GENERAL INFORMATION:
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OTHER INFORMATION: n= a,g,c or
j-09-269-939A-41
                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local :
APPLICANT: Bihain, Bernard
APPLICANT: Bougueleret, Lydie
APPLICANT: Yen-Potin, Frances
TITLE OF INVENTION: LSR Recept
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LOCATION: 21635
OTHER INFORMATION: diverging insertion,
NAME/KEY: Misc_Feature
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LOCATION: 21476
OTHER INFORMATION: diverging nucleotide,
NAME/KEY: Misc_Feature
LOCATION: 21588
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OTHER INFORMATION: diverging deletion, J
NAME/KEY: Misc Feature
LOCATION: 21270
LOCATION: 21270
OTHER INFORMATION: diverging nucleotid,
NAME/KEY: Misc Feature
LOCATION: 21356
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LOCATION: 17169
OTHER_INFORMATION: diverging nucleotide,
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OTHER INFORMATION: Potential variant
NAME/KEY: Misc_Feature
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OTHER INFORMATION: diverging deletion,
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OTHER INFORMATION: diverging deletion,
NAME/KEY: Misc_Feature
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OTHER INFORMATION: diverging mucleotide,
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OTHER INFORMATION: diverging deletion, G in
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LOCATION: 16732
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l Similarity 54.1%;
80; Conservative
                                                                                                                                                                                                                       CCCCTCCCGGCGCCACTGGCCGGTGCCC 178
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                                                                                                                                                                                                                                                                                                                                                                                                              Score 39.2;
Pred. No. 1.
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   Its Cloning and Its Application
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To

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Sequence 1, Application US/09499522
Patent No. 6479238
GENERAL INFORMATION:
APPLICANT: Blumenfeld, Maxta
APPLICANT: Bougueleret, Lydie
APPLICANT: Bihain, Bernard
TITLE OF INVENTION: POLYMORPHIC MARKERS OF TH
FILE REFERENCE: GENSET.053AUS
CURRENT APPLICATION NUMBER: US/09/499,522
CURRENT FILING DATE: 2000-02-10
EARLIER APPLICATION NUMBER: US 60/119,592
EARLIER APPLICATION DESCRIPTION SERVICES OF TH
EARLIER APPLICATION NUMBER: US 60/119,592
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JS-09-499-522-1/c
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SOFTWARE: PAIL
SEQ ID NO 19
FUNGTH: 22976
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CURRENT FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: FR 97/10086
PRIOR FILING DATE: 1997-08-06
PRIOR APPLICATION NUMBER: FR 98/05032
PRIOR APPLICATION NUMBER: FR 98/05032
PRIOR FILING DATE: 1998-04-22
NUMBER OF SEQ ID NOS: 41
SOFTWARE: Patent.pm
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nes 80; Conserv
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APPLICATION NUMBER: US 60/144,784
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19956..19958
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Pred. No. 1.8;
0; Mismatches
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                                                                                                                                                                                                                          THE LSR GENE
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SOFTWARE: Patent.pm
SEQ ID NO 1
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                                                                                           PEATURE:
PEATURE:
NAME/KEY: primer bind
1047..1068
                                                                                                                                                                                                     NAME/KEY: misc feature
LOCATION: 22324..23187
OTHER INFORMATION: homology
                                                                                                                                                                                                                                                                        PEATURE:
NAME/KEY: misc feature
TOTATION: 1..2000
TOTATION: not
                                             NAME/KEY: primer_bind
LOCATION: 946..963
                                                                               LOCATION: 1047..1068
OTHER INFORMATION: downstream
NAME/KEY: primer_bind
                          OTHER INFORMATION: upstream amplification primer 99-4576
                                                                                                                                       LOCATION: 523..544
OTHER INFORMATION: upstream amplification primer 17-2
                                                                                                                                                              NAME/KEY: primer_bind
LOCATION: 523..544
                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                  LOCATION: 1..2000
OTHER INFORMATION: potential
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OTHER INFORMATION:
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LOCATION: 12163..12
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                            NAME/KEY: polyA_signal
LOCATION: 21168..21173
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OTHER INFORMATION: exon8
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LOCATION: 20056..20187
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NAME/KEY: exon
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OTHER INFORMATION: exon7
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DTHER INFORMATION: exon6
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OTHER INFORMATION:
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                                                                                     amplification
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                                                                                     primer 17-2 , complement
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FEATURE:

NAME/KEY: primer bind

TOTATION: 1096...1115
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NAME/KEY: primer bind

TOCATION: 3882..3901
                                                                                                                                                                                                                                LOCATION: 4336..4356
OTHER INFORMATION: downstream
                                                                                                                          NAME/KEY: primer_bind
LOCATION: 4444..4463
                                                                                                                                                                                         NAME/KEY: primer_bind LOCATION: 4902..4920
                                                                                                                                                                                                                                                   NAME/KEY: primer bind LOCATION: 4336..4356
                                                                                                                                                                                                                                                                                               LOCATION: 3775..3792
OTHER INFORMATION: upstream
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LOCATION: 3455...3474
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OTHER INFORMATION: upstream
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LOCATION: 2470..2489
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OTHER INFORMATION: downstream
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LOCATION: 2483..2500
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OTHER INFORMATION: downstream
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LOCATION: 2074..2093
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LOCATION: 1602..1621
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OTHER INFORMATION: downstream
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OTHER INFORMATION: upstream
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OTHER INFORMATION: downstream amplification primer 99-4576 , complement
                                              OTHER INFORMATION: upstream
                                                              NAME/KEY: primer_bind
LOCATION: 6638..6655
                                                                                                           OTHER INFORMATION: downstream
                                                                                                                                                                        OTHER INFORMATION: upstream
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LOCATION: 1616..1635
                   VAME/KEY:
   OCATION:
primer_bind
7072..7089
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US-09-252-991A-10838/c; Sequence 10838, Application; Patent No. 6551795
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Best Local S
Matches 80
                                         GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS A
FILE REFERENCE: 107196.136
CURRENT APPLICATION UNMERER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER:
             PRIOR APPLICATION NUMBER: US PRIOR FILING DATE: 1998-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: primer_bind
Name/KEY: 11972...11990
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NAME/KEY: primer bind

TOTATION: 10023...10040
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LOCATION: 7995..8012
OTHER INFORMATION: upstream
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LOCATION: 12481..12501
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OTHER INFORMATION: downstream
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OTHER INFORMATION: downstream
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LOCATION: 10546..1056
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OTHER INFORMATION: upstream
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LOCATION: 8576..8593
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9622..9639
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US 60/094,190
                             US 60/074,788
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                                                                                                         SEQUENCES
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                                                                                          THERAPEUTICS
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WESULT 15
US-09-252-991A-10890
Sequence 10890, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: MAIC J. Rubenfield et al.
TITLE OF INVENTION: MUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196,136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
TYPE: DNA
COEGNITAN DESIGNATIONS
COEGNITAN DESIGNAT
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; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 10838
; LENGTH: 429
; TYPE: DN: Pseudomonas aeruginosa
US-09-252-991A-10838
Search completed: April 22, 2004, 04:42:56 Job time : 110.289 secs
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Matches
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Local Similarity 51.4%; Pred. No. 0.21;
les 90; Conservative 0; Mismatches 85; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                               176 TCGCCGCGCTGGGCGGCGTCAGCGGCGAGATGTGGCGTGCCGACAAGGCCGGTCTCGGCG 235
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Result No.	Score	% Query Match	Length	D B	ID	Description
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0	567	52.3	697	4	AAK92158	8 Human
7	491	45.3	494	φ.	AAI25096	6 Probe
8	491	45.3	494	4	ABA70786	Human
9	491	45.3	494	4	AAI50961	
10	491	45.3	494	4	ABA37272	
11	491	45.3	494	4	AAK44992	Human
12	491	45.3	494	4	AAK19040	Human
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16	80.	35.1		4.	AAI15879	Probe
17	380.2	35.1	474	4	ABA58185	5
18	80.	•	474	4	AAI37794	4 Probe
19	80.		474	4	ABA27366	
20	80.	35.1	474	4	AAK31927	7 Human
21	80.		474	4	AAK06266	Human
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4.0	4.0	4.0	4.0	4.0	4.1	4.1	4.2	4.3	5 5	8.3	8.3	8.3	8 	10.4	10.4	10.4	10.4	12.3	12.3	18.2	24.5
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Aba17546	Aba17545	Abk28238	Ab133295	Aas45393	Adb87400	Ada71938	Abz17427	Ada71938	Abn37591	Abq13705	Abq13704	Abq40650	Abq40651	Abq13703	Abq13702	Abq40652	Abq40653	Ab168165	Ab166053	Ab179601	Abq55979
Human ner	Human ner	DNA trans	Human imm					Rice gene	Human spl		Oligonucl	Kidney ca	Lung canc	Human ova	Human ova						

ALIGNMENTS

RESULT 1 AAXO2855 ID AAXO XX Secur KW hypo XX Reig KW Reig KW Reig KW Cher XX Homo XX WO99 XX WO99 XX WO99 XX U099 XX U099 XX U099 XX U099 XX U099 XX WO99 XX WO99 XX WO99 XX U099 XX U099 XX U099 XX WO99 XX U099 XX Secreted protein; zsig46; human; chromosome 13; thyroid; disease; hypothyroidism; Graves' disease; thyrocoxicosis; thyroid cancer; Hirschaprung's disease; neuronal ceroid-lipofucinosis; Wilson disease; Reiger syndrome; immunoassay; detection; anti-idiotypic antibody; 14-MAY-1999 AAX02855 standard; DNA; 1486 BP Homo sapiens. therapy; diagnostic; ss. Human zsig46 DNA. AAX02855; (first entry)

Location/Qualifiers /product= "zsig46" /*tag=

WO9905275-A1.

04-FEB-1999.

24-JUL-1998; 98WO-US015431.

24-JUL-1997; 97US-0053613P.

Sheppard PO, (ZYMO) ZYMOGENETICS INC Gilbertson DG;

WPI; 1999-142930/12. P-PSDB; AAW92967.

New secreted polypeptide, zsig46, and its fragments, related fusion proteins - used for diagnosis and treatment of thyroid disorders or diseases involving genes on chromosome 13.

Claim 27; Page 88-90; 101pp; English.

This invention describes the isolation zsig46 encoded by a gene on chromosome of a novel human secreted protein, 13 which is mainly expressed in

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the thyroid. This product can be used to study secretion of proteins from cells and also to treat or prevent deficient expression of zsig46, which may be associated with thyroid diseases (e.g. hypothyroidism, Graves' disease, thyrotoxicosis, thyroid cancer etc.) or with diseases that involve genes in the same region of chromosome 13 (e.g. Hirschsprung's disease, neuronal ceroid-lipfucinosis, Wilson disease and Reiger syndrome). Antibodies and other binding proteins, are used as immunoassay reagents to detect zsig46 or cells expressing it, e.g. for assessing thyroid function to produce anti-idiotypic antibodies, for affinity purification of zsig46, to screen expression libraries, to neutralise zsig46 activity, and to deliver toxins, radioisotopes etc. for therapeutic or diagnostic purposes. Agonists of the product can be used to promote growth, differentiation and proliferation of specific cell types, e.g. for treating (extra)thyroid diseases or as additive to cell
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                               GACCTTTAACAAGTTGGCTGAATTTTGGAGCAGAGTTCAAGAACATAGAAACCAACTATAC
                                                                                                                   CCCAGAAAAGGGGGCAGAGACATGGTTTGATTCCTACGACTGTTCCAAATTTTGTGTTAAG
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Feng P, Soppet R, Lafleur DW,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; ds; immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS; cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus; osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human secreted protein gene 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
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98US-0078578P.
98US-0078579P.
98US-0078581P.
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98US-0080314P.
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Matches 1067;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence represents a nucleic acid molecule which encodes a secreted human protein. The gene number, and the clone it is derived from, are detailed in the descriptor line. The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin Fc portion (e.g. AAZ24802) for increasing the stability of the fused protein as compared to the human protein only. The invention relates to 95 novel genes and their fragments (nucleic acid sequences: AAZ24811-Z24907; amino acid sequences AAY41308-Y41404) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the amount of the new polymeptides in a sample or by determining the presence of mutations in the new polymucleotides. Specific uses are described for each of the 95 polymucleotides, based on which tissues they are most highly expressed in (see AAZ24811 for described uses)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1751 BP;
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  GTTCAAGTAGCAACTATATCAGGAAACATGTTCAACCAAATGGCAAAGTGGGTGAAACAG
                                                                                                                                                                            GGCAACTGTACATTTCCCCCATCTCCGACCTGAAATGGATGCCCCTTTCTGGTGTAATCAA
                                                                                                                                                                                                                                                                                                             GGCAACTGTACATTTCCCCATCTCCGACCTGAAATGGATGCCCCTTTCTGGTGTAATCAA 4.33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     for diagnosis and treatment of e. immune diseases, inflammation or
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clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers

The invention relates to primers for synthesising full length

SEQ ID NO 3977; 1380pp + Sequence Listing; English

Claim 8;

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RESULT 3
AAK94829
ID AAK9
XX AAK9
AC AAK9
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11-JAN-2000; 2000JP-00118774
02-MAY-2000; 2000JP-00183765
                                                                                                                                                                                                                                                                                                                      WPI; 20
P-PSDB;
                                                                                                                                                                                                                                           830 Primers useful for synthesizing in genetic manipulation.
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                                       This invention describes the isolation of a novel human secreted protein, comparison to the thyroid. This product can be used to study secretion of proteins from cells and also to treat or prevent deficient expression of zsig46, which compares the thyroid with thyroid diseases (e.g. hypothyroidism, Graves' disease, thyrotoxicosis, thyroid cancer etc.) or with diseases that convolve genes in the same region of chromosome 13 (e.g. Hirschaprung's disease, neuronal ceroid-lipofucinosis, Wilson disease and Reiger compares to detect zsig46 or cells expressing it, e.g. for assessing thyroid function to produce anti-idiotypic antibodies, for affinity curification of zsig46, to screen expressing it, e.g. for assessing comparistic purification and to deliver toxins, radioisotopes etc. for promote growth, differentiation and proliferation of specific cell types, e.g. for treating (extra)thyroid diseases or as additive to cell
                                                                                                                                                                                                                                                                                                                                             New secreted polypeptide, zsig46, and its fragments, related fusion proteins - used for diagnosis and treatment of thyroid disorders or diseases involving genes on chromosome 13.
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Query Match Best Local Similarity Matches 640; Conserv

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189 A; 106 C; 179 G;

166 T; 0 U;

71.3%; Score 772.4; 61.7%; Pred. No. 2.4

2.4e-190;

Length 398 Other;

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Mismatches

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MODEL-frame+_D2n.model -DEV=xlh
Q=/cgn2_1/USPTO_spool/US10010050/runat_22042004_113204_27549/app_query.fasta_1.1372
Q=/cgn2_1/USPTO_spool/US10010050/runat_22042004_113204_27549/app_query.fasta_1.1372
DB=GenEmbl -QFMT=fastap -SUFFIX=+ge -MINMATCH=0.1 -LOOFEXT=0 -LOOFEXT=0
UNITS=bits -START=1 -END=-1 -MATRIX=bidosum62 -TRANS=biumar40.cdi -LIST=45
DCCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE-LOCAL
OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
USET=US10010050_GCGN_1 1 7433_Grunat_22042004_113204_27549 -NCPU=6 -ICPU=3
NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
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             April 24, 2004, 22:59:32 ; Search time 6540.36 Seconds (without alignments) 2292.945 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ZYMOGENETICS INC
OS Homo sapiens
PN JP 200151134:
PD 14-AUG-2001
PF 24-JUL-1998
PR 24-JUL-1998
PR 24-JUL-1997
PI PAUL O SHEPPI
PC C12N15/09,A6
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1 (bases 1 to 1486)
Sheppard, P.O. and Gilberton, D.G.
Secreted protein which human chromosome 13 encodes
Patent: JP 2001511345-A 1 14-AUG-2001;
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C12N1/21,C12N5/10,C12P21/02,C12Q1/68,C12N15/00,A61K37/02,C12N5/
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                      MetGluTrpTyrGluLeuPheGlnLeuGlyAsnCysThrPheProHisLeuArgProGlu
                                                                                      LeuLysIleMetHisAspAlaIleGlyPheArgSerThrLeuThrGlyLysAsnTyrThr
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JP 2001511345-A/1
14-AUG-2001
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24-UUL-1997 US 60/053613
PAUL O SHEPPARD, DIBRA G GILBERTON
C12N15/09, A61K38/00, A61K48/00, C07K14/47, C07K16/18, C12N1/15,
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Submitted (26-MAY-1998) Department of Human Molecular National Public Health Institute, Mannerheimintie 166, 00300, Finland
                                                                          2 (bases 1 to 4080)
Savukoski,M., Klocka
                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 4080)

Savukoski,M., Klockars,T., Holmberg,V., Santavuori,P., Lander,E.S and Peltonen,L.
                                              and Peltonen, L.
Direct Submission
                                                                                                                                                                               CLN5, a novel gene encoding a putative transmembrane protein mutated in Finnish variant late infantile neuronal ceroid
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                                                                              Klockars, T.,
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                                                                               Holmberg, V., Santavuori, P.,
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mRNA,

complete

Genetics, Helsinki

Lander, E.S

PRI 28-JUL-1998

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886 280 826 260 766

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PN JP 2002506627-A/25

PD 05-MAR-2002

PF 18-MAR-1999 UP 2000536733

PF 18-MAR-1999 US 60/078576,19-MAR-1998 US 60/078576 PR

19-MAR-1998 US 60/078573,19-MAR-1998 US 60/078577 PR

19-MAR-1998 US 60/078581,19-MAR-1998 US 60/078577 PR

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19-MAR-1998 US 60/078583,01-APR-1998 US 60/080314 PR

19-MAR-1998 US 60/080312,01-APR-1998 US 60/080313 PI STEVEN

M RUBEN, JIAN NI CRAIG A ROSEN,GUO

LIANG YU, PAUL E YOUNG,

PI DANIEL R SOPPET, YING FEI WEI, GREGORY A ENDRESS, ROXANNE D DUAN,

PI PING FENG,

PI A MOORE

PI A MOORE

C12N15/09,A61K38/00,A61K48/00,A61P43/00,CO7X14/47,CO7X16/18,

PC C12N1/15,

CC C12N1/19,C12N1/21,C12N5/10,C12P21/02,C12Q1/68,G01N33/53,G01N33/ PC
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Ruben,S.M., Ni,J., Rosen,C.A., Yu,G.L., Young,P.E., Fen,P. Soppet,D.R., Wei,Y.F., Endress,G.A., Duan,R.D., Kyaw,H., E Lafleur,D.W., Olsen,H.S., Shi,Y. and Moore,P.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        95 human secretory proteins
Patent: JP 2002506627-A 25 HUMAN GENOME SCIENCES INC
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95 human secretory proteins.
BD136338
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Location/Qualifiers
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/db_xref="taxon:9606"
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Roga, H.

Primer for synthesizing full-length cDNA and Patent: JP 2002017375-A 3289 22-JAN-2002;

HELIX RESEARCH INSTITUTE
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1 (Dases 1 to 2120)

Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y., Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and
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JP 2002017375-A/3289
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                                                                                                                                                                                                                                                                                                                                                                           SHINICHI KOJIMA,
                                                                                                                                                                                                                        Primer for synthesizing full-length cDNA and use thereof Location/Qualifiers (16). (1089).
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JP 2002017375-A/3289
22-JAN-2002
07-JUL-2000 JP 2000253172
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                                                                                                                                                                                                                                                                                                                                                                                          YURI KAWAI,AI WAKAMATSU,TOMOYASU SUGIYAMA,KEIICHI NAGAI,
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                                                                                                                            /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (35-MAR-2002) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction: Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center; cDNA 5'- & 3'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isogai,T., Ota,T., Nishikawa,T., Hayashi,K., Otsuki,T., Sugiyama,T., Suzuki,Y., Nagai,K., Sugano,S., Ishii,S., Kawai-Hio,Y., Saito,K., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Kojima,S., Nagahari,K., Masuho,Y., Ono,T., Okano,K., Yoshikawa,Y., Aotsuka,S., Sasaki,N., Hattori,A., Okumura,K., Iwayanagi,T. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 (bases 1 to 2120)
Isogai,T. and Otsuki,T.
Direct Submission
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LysTyrThrPheCysProThrGlySerProIleProValMetGluGlyAspAspAspIle
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/clone_lib="pLACE1"
/note="cloning vector: ]
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/mol_type="mRNA"
/db_xref="taxon:9606"
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artificial sequences.

1 (bases 1 to 1038)
Sheppard, P.O. and Gilberton, D.G.
Secreted protein which human chromosome
Patent: JP 2001511345-A 12 14-AUG-2001;
ZYMOGENETICS INC
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                                        AsnGlnMetAlaLysTrpValLysGlnAspAsnGluThrGlyIleTyrTyrGluThrTrp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism='Artificial
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.05e-139
1631.00
83.19%
83.19%
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Matches:
Conservative:
Mismatches:
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MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM
                                                                               TITLE
                                                                                                                                                                                                                                                                                            TITLE
                                                  JOURNAL
                                                                                                                                                                       PUBMED
                                                                                                                                                                                                                                                                   RS Strausberg, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, M.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodrigues, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schmerch, A., Schein, J.E., Jones, S.J. and Marra, M.A., Generation and initial analysis of more than 15,000 full-length human and monice cnum sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1021
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Direct Submission submitted (06-MAR-2002) National Institutes of Health, Mammalian Concor Consortion (MGC), Cancer Genomics Office, National Cancer
                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus ceroid-lipofuscinosis, IMAGE:5251891), partial cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GluThrAsnTyrThrArgIlePheLeuTyrSerGlyGluProThrTyrLeuGlyAsnGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAYGCNGTNATHGTNCAYAARCARTTYTAYYTNTTYTAYAAYTTYGARTAYTGGTTYYTN 960
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCNATGAARTTYCCNTTYATHAARATHACNTAYGARGARATHCCNYTNCCNATHMGNAAY 1020
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A (cDNA clone
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REMARK
COMMENT
US-10-010-050A-2 (1-346)
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                                                                                                         Best Local Similarity:
                                                                                                                                     Percent Similarity:
                                                                                                                                                               Score:
                                                                                                                                                                                           Pred. No.:
                                                                                                                                                                                                               Alignment Scores:
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Contact: nisc_mgc@nhgri.nih.gov
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Akhter,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Gupta,J., Haghighi,P.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,O.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.D., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphre
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/Lini at: http://image.lini.gov Series: IRAK Plate: 56 Row: c Column: 7
This clone was selected for full length sequencing because it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Institute, 31 Center Drive, Room 11A03, Bethesda, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaithersburg, Maryland;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the following selection criteria: Hexamer
                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="LocusID:211286"
/db_xref="MGI:2442253"
/db_xref="MGI:2442253"
/translation="TRPAHMRPALALALIGLATILGASPTSGQRWPVPYKRESERPKT
/translation="TRPAHMRPALALALIGLATILGAPIWEEKYGDLLGHFKLMHDAVGERS
DYCQAKYTECPTGSSIPVMKDNDVLEVLRLGAPIWEEKYGDLAGHFKLMHDAVGERS
TLTGKNYTIEWYELFQLGNCTFPHLRPDKSAPFWCNQGAACFFEGIDKHWKENGTLS
                                                                                                                                                                                                                                                                                               LSTKDFLMNFLKIFDTVIIHRQFYLFYNFEYWFLPMKPPFVKITYEETPLPTRHTTFT
DL"
                                                                                                                                                                                                                                                                                                                                                        VVATISGNTFNKVAEWVKQDNETGIYYETWTVRAGPGQGAQTWFESYDCSNFVLRTYK
KLAEFGTEFKKIETNYTKIFLYSGEPIYLGNETSIFGPKGNKTLALAIKKFYGPFRPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=3
/product="Cln5 protein"
/protein_id="AAH25487.1"
/db_xref="GI:19343791"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="Cln5"
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old, gross tissue."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:10090"
/clone="IMAGE:5251891"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'gene="Cln5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             db_xref="MGI:2442253"
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1451.00
85.76%
76.56%
75.30%
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BC025487 (1-2318)
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Matches:
                                                                                                            Mismatches:
                                                                                                                                  Conservative:
                                                                                  Indels:
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12 AlaSerTrp-----CysTrpAlaLeuAlaLeuLeuTrpLeuAlaValValProGlyTrp

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DEFINITION
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LOCUS
  TERSION
                    ACCESSION
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                                                       AC109554 198524 bp DNA linear HTG 11-OCT-2002 Rattus norvegicus clone CH230-331D3, *** SEQUENCING IN PROGRESS
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AC109554.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GlyAlaAlaCysPhePheGluGlyIleAspAspValHisTrpLysGluAsnGlyThrLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PheArgSerThrLeuThrGlyLysAsnTyrThrMetGluTrpTyrGluLeuPheGlnLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGGGAATTTAAATATGGAGACCTCCTGGGACACTTTAAACTTATGCATGACGCCGTGGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AlaGluThrTrpPheAspSerTyrAspCysSerLysPheValLeuArgThrPheAsnLys 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCAGTCGTTGCAACCATATCCGGAAACACATTTAACAAAGTGGCCGAGTGGGTGAAGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ValGlnValAlaThrIleSerGlyAsnMetPheAsnGlnMetAlaLysTrpValLysGln 189
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                                                                                                                                                                                                                                                                                                                                                                               LysGluPheLeuLeuSerLeuLeuGlnTlePheAspAlaValTleValHisLysGlnPhe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LeuAlaGluPheGlyAlaGluPheLysAsnIleGluThrAsnTyrThrArgIlePheLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGCAACTGTACATTTCCCCACCTCCGGCCTGACAAGAGCGCTCCCTTCTGGTGTAACCAA
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                                                                                                                                                                                       ThrTyrGluGluIleProLeuProIleArgAsnLysThrLeuSerGlyLeu 346
                                                                                                                                                                                                                                                                                 TyrLeuPheTyrAsnPheGluTyrTrpPheLeuProMetLysPheProPheIleLysIle
                                                                                                                                                                                                                                                                                                                                         AAGACTCTTGCTTTGGCCATAAAAAATTTTATGGCCCCTTCAGACCGTATTTGTCAACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                             LysThrLeuGlyLeuAlaIleLysArgPheTyrTyrProPheLysProHisLeuProThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TACAGTGGAGAGCCTATTTACCTGGGAAATGAAACATCTATTTTTGGGCCCCAAAGGAAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GACAATGAAACTGGGATTTATTATGAGACATGGACGGTCCGAGCCGGCCCAGGACAAGGG
                                                                                                                                                                   ACATACGAAGAAACCCCGTTACCTACCCGACATACAACATTTACCGACTTG 1010
                                                                                                                                                                                                                                                      TACTTGTTTTATAACTTTGAGTATTGGTTTCTACCAATGAAACCCCCCTTTGTCAAAATA
  GI:23820683
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Rattus norvegicus
                                                                                                                                                                                                                                                                       Submitted (05-FBB-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 198524)
Rat Genome Sequencing Consortium.
Submitted (11-OCT-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA.
On Oct 11, 2002 this sequence version replaced gi:21738217. The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Worley, K.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished
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ist Local Similarity:
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                                                                                                                                 ery Match:
                                                                                                                                                                                                                                                                                                                                                                      misc_feature
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38632 GGTGGAGCGCACTGGCGCCAGGCGCTCGCGCTACTGGGGGCTGGCGGCCACTCTG 38573
                                                                                                                                                                                                                                   Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (http://www.hgsc.bcm.tmc.edu/projects/rat/). Bach contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 table.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    by the finished sequence as soon as it is available the accession number will be preserved.

1 198524: contig of 198524 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft data.)
NOTE: This is a "working draft' sequence. It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.
This sequence will be replaced
                      GlyArgAlaSerTrp-----CysTrpAlaLeuAlaLeuLeuTrpLeuAlaValValPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center clone name: CH230-331D3
------ Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 177481 bases at least Q40
Consensus quality: 179640 bases at least Q20
Consensus quality: 18141 bases at least Q20
Consensus quality: 18141 bases at least Q20
Consensus quality: 18149 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
------ Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center: Baylor College of Medicine Center code: BCM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center project name: GQLY
                                                                                                                                                                                                                                                                                         end_sequence:RXAPC14TV"
                                                                                                                                                                                                                                                                                                                 site:MboI
                                                                                                                                                                                                                                                                                                                                                    end_sequence:RXAPC14TJ"
197370. .198217
/note="clone_boundary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="clone_boundary
clone_end:T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="wgs_end_extension
clone_end:T7"
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Matches:
Conservative:
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                                                                                                                                                                                                                                                                                                    AAAATAACGTACGAGGAAACCCCTTTACCTACCCAACATACGACATTTACCGACCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAAGGGGCGCAGACATGGTTTGAATCCTACGACTGTTCGAATTTTGTCTTAAGGACATAT 37985
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                                                                                              Submitted (13-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On May 13, 2003 this sequence version replaced gi:22855855. The sequence in this assembly is a combination of BAC based reads
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                                                                                                                                                                                                                                                                                                                      Submitted (23-JAN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 227920)
Rat Genome Sequencing Consortium.
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and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas
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Direct Submission
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Best Local Similarity:
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                                                                                                                28 GlyTrpSerArgValSerGlyIleBroSerArgArgHisTrpProValProTyrLysArg 47
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shotgun sequence only contigs will be indicated in the feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.h NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs: The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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222227. .223559
/note="wgs_contig"
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/db_xref="taxon:10116"
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85.31%
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                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebra Mammalia; Eutheria; Primates; Catarrhini; Homini 1 (bases 1 to 697)
Ota, T., Nishikawa, T., Isogai, T., Hayashi, K., Ish Wakamatsu, A., Sugiyama, T., Nagai, K., Kojima, S.,
                                                                                                                                                                                                                                Primer for synthesizing
BD125187
BD125187.1 GI:23220132
JP 2002017375-A/618.
Prīmer for synthesizing full-length cDNA
Patent: JP 2002017375-A 618 22-JAN-2002;
HELIX RESEARCH INSTITUTE
OS Homo sapiens (human)
                                                                                                                                                                                            Homo sapiens (human)
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full-length
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PD 22-JAN-2002

PF 07-JUL-2000 JP 2000253172

PF 07-JUL-2000 JP 2000253172

PI TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAYASHI, SHIZU

PI ISHII,

PI VURI KAWAI,AI WAKAMATSU, TOMOYASU SUGIYAMA, KEIICHI NAGAI, PI

SHINICHI KOJIMA,

PI TETSUJI OTSUKI, HISASHI KOGA

PC
C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/
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Primer for synthesizing full-length cDNA and use thereof FH F
Location/Qualifiers
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                        TCAACCAAATGGCAAAAGTGGGTGAAACAAGGACAATNGAAACAAGGAATTTATTATGAG
                                                 <u>AIGGAATGGTATGAACTTTTCCAACTTGGCAACTGTACATTTCCCCATCTCCGACCTGAA</u>
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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                                                                                   172
                                                                                                                                          112
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BD126453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HELIX RESEARCH INSTITUTE

OS Homo sapiens (human)

PN JP 2002017375-A/1884

PD 22-JAN-2002

PT 07-JUL-2000 JP 2000253172

PT TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAYASHI, SHIZU

PI ISHII,

PI YURI KAWAI, AI WAKAMATSU, TOMOYASU SUGIYAMA, KEIICHI NAGAI, PI

SHINICHI KOJIMA,

PI TETSUJI OTSUKI, HISASHI KOGA

PC

C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/
                                                     61
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                                                                                                                                                                                                   52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Primer for synthesizing full-length cDNA and use thereof Patent: JP 2002017375-A 1884 22-JAN-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ota,T., Nishikawa,T., Isogai,T., Hayashi,K.,
Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 697)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (human)
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                                                                                                                                                                                                                       MetArgArgGlyAlaGlyAlaAlaArgGlyArgAlaSerTrpCysTrpAlaLeuAlaLeu
                                                                                                                                                            LeuTrpLeuAlaValValProGlyTrpSerArgValSerGlyIleProSerArgArgHis
                                               LysTyrThrPheCysProThrGlySerProIleProValMetGluGlyAspAspAspIle
                                                                                     TGGCCGGTGCCCTGCAAGCGCTTTGACTTCCGTCCAAAACCTGATCCTTATTGTCAAGCT
                                                                                                    TrpProValProTyrLysArgPheAspPheArgProLysProAspProTyrCysGlnAla
                                                                                                                                            CTTTGGCTCGCGGTTCCGGGCTGGTCCCGGGTCTCGGGCATCCCCTCCCGGCGCCAC
                                                                                                                                                                                                   ATGCGGCGGGGCGCGCCTCGGGGACGCGCTTCCTGGTGCTGGGCCCTGGCGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -ThrTrpAsnValLysAlaSerProGluLys---GlyAlaGlu
GluValPheArgLeuGlnAlaProValTrpGluPheLysTyrGlyAspLeuLeuGlyHis 100
                            AAGTATACTTTCTGTCCAACTGGCTCACCTATCCCAGTTATGGAGGGTGATGATGACACT 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C12P21/02,C12Q1/68//C12P21/08,G06F17/30,C12N15/00,C12N5/00 C0mer for synthesizing full-length cDNA and use thereof FH Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      for synthesizing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism='Homo
                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/mol_type="genomic DNA"
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Kojima,S., Otsuki,T. and
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    repeats were identified using RepeatMasker: Smit, A.F.A. &
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AC001226 106988 bp
Genomic sequence from Human 13,
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1 (bases 1 to 106988)
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Submitted (29-MAY 1997) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On May 29, 1997 this sequence version replaced gi:1932720. The Staden databases, finishing information, and all chromatographic files used in the assembly of this clone are available from our anonymous ftp site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (10-APR-1997) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
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repeat_region complement(5016050186) /rpt_family="Af_rich" repeat_region 5095251121 /rpt_family="MER5A" repeat_region complement(5214052284) /rpt_family="AlluJo"	complement (47612 /rpt family="(CATA) complement (47946 /rpt family="Aludo" complement (49827 /rpt family="AT_ric	/rpt 44544 /rpt /rpt compl /rpt /rpt /rpt	t_region t_region t_region t_region t_region	repeat_region 40945. 41663 repeat_region 40945. 41663 repeat_region 40042. 42352 repeat_region 40042. 42352 repeat_region 40045. 42352 repeat_region 4267. 42771 repeat_region 42772. 42848 repeat_region 42772. 42848	region 31487 rpt region compl region /rpt region 35070 region 35070 region compl region compl	region 2 region 2 region 2 region 2 region 2 region 3 region 3	repeat_region complement(2038920494) repeat_region 2.0194 repeat_region 2.0194 repeat_region 2.0194 repeat_region 2.0194 repeat_region complement(2333123353)

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RESULT 13
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                                                      Homo sapiens (human)
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                       Homo sapiens chromosome 13 clone RP11-185124, 14 unordered
                                                                                          HTG; HTGS_PHASE1; HTGS_CANCELLED
                                                                                                                     AL136440.2 GI:10039473
                                                                                                                                        AL136440
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PheGlyAlaGluPheLysAsnIleGluThrAsnTyrThrArgIlePheLeuTyrSerGly 252
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                                                                                                                                                                                                                                                          GAAATCCCTTTACCTATCAGAAACAAAACACTCTCTGGTTTA 32375
                                                                                                                                                                                                                                                                                        GluIleProLeuProIleArgAsnLysThrLeuSerGlyLeu 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                        LeuLeuSerLeuLeuGlnIlePheAspAlaValIleValHisLysGlnPheTyrLeuPhe
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/rpt_family="(TGAA)n"
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complement(54755, .54782)
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      misc_feature
                                                                                  misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 162085 bases at least Q40
Consensus quality: 164521 bases at least Q30
Consensus quality: 166040 bases at least Q20
Insert size: 168062; sum-of-contigs
Insert size: 168062; sum-of-contigs
Insert size: 164956; 1.7% error; agarose-fp
Quality coverage: 4.08x in Q20 bases; sum-of-contigs Quality
coverage: 4.16x in Q20 bases; agarose-fp
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On Sep 8, 2000 this sequence version replaced gi:6982057.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center project name: bA185I24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     consists of 14 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 as soon as it is available and the accession number will be preserved.
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                                          /note="assembly_fragment:00318
clone_end:T7
                  vector_side:left"
                                                                                                                                                                                                        organism="Homo sapiens"
                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                         crone_
                                                                                                                              clone="RP11-185I24"
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                                                                                                                                                                                                                                                                67720: gap of 100 bp
93413: contrig of 25693 bp in length
93513: gap of 100 bp
114081: contrig of 20568 bp in length
114181: gap of 100 bp
126206: contrig of 12025 bp in length
126306: gap of 100 bp
144583: contrig of 18277 bp in length
144683: gap of 100 bp
147136: contrig of 2453 bp in length
147236: gap of 100 bp
16925: contrig of 17689 bp in length
16925: gap of 100 bp
169362: contrig of 4337 bp in length
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                                                                                                                                                    CysPhePheGluGlyIleAspAspValHisTrpLysGluAsnGlyThrLeuValGlnVal 172
  GAACCTACTTATCTGGGAAATGAAACATCTGTTTTTGGGCCAACAGGAAACAAGACTCTT
                      GluProThrTyrLeuGlyAsnGluThrSerValPheGlyProThrGlyAsnLysThrLeu
                                                                        PheGlyAlaGluPheLysAsnIleGluThrAsnTyrThrArgIlePheLeuTyrSerGly
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16545. .19514
/note="assembly_fragment:00157
fragment_chain:1"
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67721. .93413
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144684. .147136
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114182. .126206
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165026. .169362
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fragment_chain:1"
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fragment_chain:2
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fragment_chain:2"
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fragment_chain:2"
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118598 GGTTTAGCCATAAAAAGATTTTATTACCCCCTTCAAACCACATTTGCCCAACTAAAGAATTT
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AL359875
AL359875.3 GI:9864226
HTG: HTGS PHASE1; HTGS CANCELLED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Insert size: 245987; sum-of-contigs
Insert size: 190986; agarose-fp
Quality coverage: 2.52x in Q20 bases; sum-of-contigs Quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Assembly program: XGAP4; version 4.5
Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; 100752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 230299 bases at least Q30
Consensus quality: 234299 bases at least Q30
Consensus quality: 241103 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (12-JUN-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Aug 22, 2000 this sequence version replaced gi:8894433.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (human)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                             NOTE: This is a 'working draft' sequence. It currently consists of 53 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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2231
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5790
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10147
12625
12725
20994
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    28937
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2230:
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contig of 2130 bp in 1
gap of 100 bp
contig of 3459 bp in 1
gap of 100 bp
contig of 4257 bp in 1
gap of 100 bp
contig of 2478 bp in 1
gap of 100 bp
contig of 2478 bp in 1
gap of 100 bp
contig of 7843 bp in 1
gap of 100 bp
contig of 7843 bp in 1
gap of 100 bp
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_	4464 194563: gap o	
misc_teature	194463: contig of	
•	189602: contig of 189702: gap of 10	
misc_feature	187238: contig of 2223 bp in i 187338: gap of 100 bp	
ı	184915: CONCID OF 12915 NO 111	
misc feature	171996: gap of 100 bp	
į	166700: gap or 10 171896: contig of	
misc feature	166600: contig of	
misc_feature	164334: contig of	
	160153: contig of 160253: gap of 10	
misc_feature	157022: gap of 100 bp	
	152358: gap of 100 bp	
misc_feature	148866: gap of 152258: contiq	
٠.	143892: gap or 100 148766: contig of	
miso feature	* 132133 137222: 940 or 100 up * 132233 137792: contig of 11560 bp in length	
misc_feature	132132: contig of	
	129684: contig c	
misc_feature	127087: contig of 10	
	123630: gap of 100 bp	
misc_feature	118693: gap of 1 123530: contig	
	118593: contig of	
misc feature	115555: contig of	
misc_teature	110871: contig of 10	
	104059: gap of 10	
misc_feature	100692: gap of 100 bp	
	95719: gap of 10 100592: contig of	
misc_feature	95619: contig c	
	93380: contig of	
	89150: contig of	
	85667: gap of 100 bp	
source	75129: gap of 100 bp	
	68040: gap of 10 75029: contig of	
* *	67940: contig of	
* *	65281: contig c	
* *	63088: contig of	
*	56543: CONCIS OF 41/4 DP III I	
* *	52269: gap of 100 bp	
**	48520: gap or ro 52169: contig of	
* * 21	48420: contig of 8	
* * 20	40245: contig of 2	
* 200	37649: contig c 37749: gap of 1	
	35153: contig of 2823 bp in 35253: gap of 100 bp	
* *	32330: gap of 100 bp	
* 19	3030: contig of 3194	

/note="assembly fragment:01219 fragment chain:1" 5790. 10046 /note="assembly fragment:00352 fragment_chain:1" fragment_chain:1" 100547 /note="assembly fragment:00547 fragment_chain:2" fragment

/note="assembly fragment:00469 fragment_chain:1" 2231. .5689

/note="assembly fragment:00606 fragment_chain:3" 32331. 35153 /note="assembly fragment:01016 fragment chain:3" 35254. 37649

/note="assembly_fragment:01277 fragment_chain:3" 3750. .40245 /note="assembly_fragment:00920 fragment_chain:4" 40346. .48420 /note="assembly_fragment:01288 fragment_chain:4" 48521. .52169 /note="assembly_fragment:00615 fragment_chain:4" 52270. .56443 /note="assembly_fragment:0009 fragment_chain:5" 56544. .63088 /note="assembly_fragment:00448 fragment_chain:5"

63189. .65281 /note="assembly_fragment:00027

misc_feature				source	EATURES																	•			
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2130 note-"assembly fragment:00469	chromosome="13" clone="RP11-453N22" clone_lib="RPCI-11.	xref="taxon:96	/mol type="genor	. 251187	ation/Qua	251187:	241058:	240958:	235042:	234942:	232710:	232610:	230127:	230027:	225345:	225245:				206237:	204160:	••	:8881	01788:	197782:
mhlv fr	="13" 1-453N2; "RPCI-1;	. 96	3		alifiers	contig	gap of	contig	gap of	contig	gap of	contig	gap of	contig	gap of		gap of	contig	gap of	contig	gap of	contig	gap of	contig	gap of
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						length.		length		length		length		length		in length		length		length ·		length		length	

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Sequence split into (
Fragment Name
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AE014175_1
AE014175_2
AE014175_3
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                                        AUTHORS
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                                                                                                                                                                                         complete
AE014175
                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 404829)
                    Peterson,K., King,B., Hagge-Greenberg,A., Roix,J.,
O'Brien,T.
                                                                                                                                                                                                                           Mus musculus piebald
Functional and comparative genomic analysis of the piebald deletion
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GluIleProLeuProIleArgAsnLysThrLeuSerGlyLeu 346

        CTGTTGAGCCTTGCAAATTTTTGATGCAGTGATTGTGCACAAACAGTTCTATTTGTTT

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The strings of n's in this record represent gaps between contigs, and the length of each string corresponds to the length of the gap except where there are 20 n's. A string of 20 n's represents a gap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             region of mouse chromosome 14
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Adams, M. and Mural, R.
Direct Submission
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/gene="Cln5"
join(<61259. .61</pre>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="Fbl3a" / product="leucine-rich repeat-containing FBL3A"
                                                                                                                                                                                                                                                                                                               /tranelation="rmkrggrdsdqdsaeegtaekkkrrttqersqpcdwgnllqdi
vlhyekylpildrahasqucamwqvehmpdlwrceepelnopatsyllathepelko
iikrhenhlqyvsfkvdsskesaeacdilsqlvungskthiglistarpsfwdlpksh
fisaltyvfvnskslsskiddtpuddpslkylvannsdtlkilkmsscphyspagil
cvadqchglrelalnyhilsdelllalssekhyrlehlridvsenpgqthfhtiqks
swdafikhspkvnluwyfflyeeefdpffreifpathlyfgrsvskyvlgrvgntchr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement (<73858. .>86476)
/gene="Fb13a"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="ceroid-lipofuscinosis, neuronal 5"
/note="partial transcript derived from alignment
tentative consensus sequence TC227789, from TIGR
Gene Index (v. 6.0)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement (join (<73858. .74501, 80293. .80464, 83295. .83417,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66916. .>68607)
                                                                                                                    /note="PAM, protein associated with Myc; partial transcript derived from alignment of Homo sapien RefSeq sequence NM_015057"
                                                                                                                                                                                                                                                                           LVELVVCANGLRELLERIAERCKNLSAIGLGECEVSCSAFVEFVKMCGGRLSQLS
IMEEVLIPDQKYSLEQIHWEVSKHLGRVWFPDMMPTW"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement (join (73858. .74501, 80293.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="Irg1"
<38137. .>47%
                                                                                                                                                                                                                                                     complement (<106136. .>339446)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="immuneoresponsive gene 1"
/note="partial transcript sequence derived from alignment
to GenBank Accession Number L38281"
                                                                                                                                                                                                               complement (<106136. .>339446)
                                                                                                                                                                                                                                                                                                                                                                                                                                /protein_id="AAM92567.1"
/db_xref="GI:22128030"
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'db_xref="taxon:10090"
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                                                                                                                                                                                               'gene="Phr1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      product="leucine-rich repeat-containing
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CCTACCCGACATACAACATTTACCGACTTG	337 ProIleArqAsnLysThrLeuSerGlyLeu 346	67335 TATTGGTTTCTACCAATGAAACCCCCCTTTGTCAAAATAACATACGAAGAAACCCCGTTA	317 TyrTrpPheLeuProMetLysPheProPheIleLysIleThrTyrGluGluIleProLeu	- 5-	297 LeuGlnIlePheAspAlaValIleValHisLysGlnPheTyrLeuPheTyrAsnPheGlu	CCGTATTTGTCAACCAA	277 LysArgPheTyrTyrProPheLysProHisLeuProThrLysGluPheLeuLeuSerLeu	67155 CTGGGAAATGAAACATCTATTTTTGGGCCCAAAGGAAACAAGACTCTTGCTTTGGCCATA	257 LeuGlyAsnGluThrSerValPheGlyProThrGlyAsnLysThrLeuGlyLeuAlaIle	67095 TTCAAGAAGAAACAAACTATACGAAAATATTTCTTTACAGTGGAGAGCCTATTTAC	237 PheLysAsnIleGluThrAsnTyrThrArgIlePheLeuTyrSerGlyGluProThrTyr	67035 TACGACTGTTCGAATTTTGTCTTAAGGACATATAAGAAATTGGCTGAATTTGGAACAGAA	217 TyrAspCysSerLysPheValLeuArgThrPheAsnLysLeuAlaGluPheGlyAlaGlu	66975 TATGAGACATGGACGGTCCGAGCCCGGCCCAGGACAAGGGGCCCAGACGTGGTTCGAGTCC	197 TyrGluThrTrpAsnValLysAlaSerProGluLysGlyAlaGluThrTrpPheAspSer	66915 GGAAACACATTTAACAAAGTGGCCGAGTGGATGAAGCAGGACAATGAAACTGGGATTTAT		010-050A-2 (1-346) x AE014175_0 (1-110000)	Local Similarity: 74.71% Mismatches: 21 7 Match: 37.88% Indels: 0 10 Gaps: 0
		CCCGTTA 67394	eProLeu 336	crrrcad 67334	nPheGlu 315	GAATTTC 67274	uSerLeu 295	GGCCATA 67214	uAlaIle 275	TATTTAC 67154	oThrTyr 256	AACAGAA 67094	yAlaGlu 236	CGAGTCC 67034	eAspSer 216	GATTTAT 66974	YIleTyr 196		

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DB=GenEmbl -QFWT=fastap_SUFFIX=rye -MINMATCH=0.1 .LOOPCL=0 -LOOPEXT=0
UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
DOCALLGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
DUTFWT=pto -NORM=ext -HEASIZE=500 -MINLEN=0 -MAXLEN=200000000
USER=US10010050 @CGN 1 1 7433 @runat_22042004 113204_27549 -NCPU=6 -ICPU=3
NO_MARP -LARGEQUERY -NEG_SCORES=0 -MAIT -DSPELOCK=100 -LONGLOG
DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XCAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
PGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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OS Homo sapiens
PN JP 20151134
PD 14-AUG-2001
PF 24-JUL-1998
PR 24-JUL-1997
PR 24-JUL-1997
PR 24-JUL-1997
PG C12N15/09,A63
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BD073402
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Secreted protein which human chromosome 13
Patent: JP 2001511345-A 1 14-AUG-2001;
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JP 2001511345-A/1.
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C12N1/21, C12N5/10, C12P21/02, C12Q1/68, C12N15/00, A61K37/02, C12N5/ PC
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                                                                                                                                                                                                                                  ArgProLysProAspProTyrCysG1nAlaLysTyrThrPheCysProThrGlySerPro
                                                                                                                                                                                                                                                               CGGGTCTCGGGCATCCCCTCCCGGCGCCACTGGCCGTGCCCTACAAGCGCTTTGACTTC
                                                                                                                                                                                                                                                                                ArgValSerGlyI1eProSerArgArgHisTrpProValProTyrLysArgPheAspPhe
                                                        AsnCysThrPheProHisLeuArgProGluMetAspAlaProPheTrpCysAsnGlnGly
                                                                                                                                                 GlupheLysTyrGlyAspLeuLeuGlyHisLeuLysIleMetHisAspAlaIleGlyPhe
                                                                                                                                                                                                                     CGTCCAAAACCTGATCCTTATTGTCAAGCTAAGTATACTTTCTGTCCAACTGGCTCACCT
               AlaAlaCysPhePheGluGlyIleAspAspValHisTrpLysGluAsnGlyThrLeuVal
                                                                                                     ArgSerThrLeuThrGlyLysAsnTyrThrMetGluTrpTyrGluLeuPheGlnLeuGly
                                                                                                                             GAATTTAAATATGGAGACCTCCTGGGACACTTGAAAATTATGCATGATGCCATTGGATTC
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 AACTGTACATT
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24-JUL-1997 US 60/053613
PAUL O SHEPPARD DIBRA G GILBERTON
C12N15/09,A61K38/00,A61K48/00,C07K14/47,C07K16/18,C12N1/15,
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JP 2001511345-A/1
14-AUG-2001
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protein which human
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 4080)

Savukoski, Klockars, T., Holmberg, V., Santavuori, P., Lander, E.S.
                                                                                                                                                                                                                                                                                                                                                                                                     CLN5, a novel gene encoding a putative transmembrane protein mutated in Finnish variant late infantile neuronal ceroid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                      Submitted (26-MAY-1998) Department of Human Molecular Genetics, National Public Health Institute, Mannerheimintie 166, Helsinki 00300, Finland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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Savukoski, M., K
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/mol type="mRNA"
/db_xref="taxon:9606"
/chromosome="13"
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/map="13q22"
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SerGlyGluProThrTyrLeuGlyAsnGluThrSerValPheGlyProThrGlyAsnLys
                                                                                                                              GluThrTrpPheAspSerTyrAspCysSerLysPheValLeuArgThrPheAsnLysLeu
                                                                                                                                                                                          AsnGluThrGlyIleTyrTyrGluThrTrpAsnValLysAlaSerProGluLysGlyAla 180
                                                                                                                                                                                                                                                      GlnValAlaThrIleSerGlyAsnMetPheAsnGlnMetAlaLysTrpValLysGlnAsp 160
                                                                                                                                                                                                                                                                                                                          AlaAlaCysPhePheGluGlyIleAspAspValHisTrpLysGluAsnGlyThrLeuVal 140
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                                                                    AlaGluPheGlyAlaGluPheLysAsnIleGluThrAsnTyrThrArgIlePheLeuTyr
                                                                                                             GAGACATGGTTTGATTCCTACGACTGTTCCAAATTTGTGTTAAGGACCTTTAACAAGTTG
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SYDCSKFVLRTFNKLAEFGAEFKNIETNYTRIFLYSGEPTYLGNETSVFGPTGNKTLG
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TGCSLMagevDTaggaemrrgagaargraswcwalallwlavvpgwsrvsgipsrrhw
pvpykrfdfrpkpdpycgakytfcptgspipvmggdddievfrlgapvwgfkygdllg
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PN JP 200250627-A/25
PD 05-MAR-2002
PF 18-MAR-1999 US 60/078565,19-
PF 19-MAR-1998 US 60/078579,19-MAR-1
19-MAR-1998 US 60/078579,19-MAR-1
19-MAR-1998 US 60/078563,01-APR-1
19-MAR-1998 US 60/078561,000

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10-ANG-1998 US 60/078561,19-MAR-1

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Patent: JP 2002506627-A 25 05-MAR-2002;
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Ruben,S.M., Ni,J., Rosen,C.A., Yu,G.L., Young,P.E., Fen,P
Soppet,D.R., Wei,Y.F., Endress,G.A., Duan,R.D., Kyaw,H., 1
Lafleur,D.W., Olsen,H.S., Shi,Y. and Moore,P.A.
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JP 2002506627-A/25.
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Mammalia; Eutheria; Primates;
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secretory proteins.
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                                                                                                                                                                                                  SerGlyGluProThrTyrLeuGlyAsnGluThrSerValPheGlyProThrGlyAsnLys 240
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                                         LeuPheTyrAsnPheGluTyrTrpPheLeuProMetLysPheProPheIleLysIleThr 300
                                                                                           GluPheLeuLeuSerLeuLeuGlnIlePheAspAlaValIleValHisLysGlnPheTyr 290
                                                                                                                            <u>ACTOTTGGTTTAGCCATAAAAAGATTTTATTACCCCTTCAAACCACATTTGCCAACTAAA</u>
                                                                                                                                                    ThrLeuGlyLeuAlaIleLy8ArgPheTyrTyrProPheLy8ProHisLeuProThrLy8 250
                                                                                                                                                                                                                                                                                         GAGACATGGTTTGATTCCTACGACTGTTCCAAATTTGTGTTAAGGACCTTTAACAAGTTG
                                                                             GAATTTCTGTTGAGTCTCTTGCAAATTTTTGATGCAGTGATTGTGCACAAACAGTTCTAT
                                                                                                                                                                                    AGTGGAGAACCTACTTATCTGGGAAATGAAACATCTGTTTTTGGGCCAACAGGAAACAAG
TyrGluGluIleProLeuProIleArgAsnLysThrLeuSerGlyLeu 316
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RESULT 4
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OS Homo sapiens (human)
PN JP 2002017375-A/3289
PD 22-JAN-2002
PF 07-JUL-2000 JP 200253172
PF 170SHLO TPA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAYASHI, SHI ISHII, PI YURI KAWAI, AI WAKAMATSU, TOMOYASU SUGIYAMA, KEIICHI NAGAI, PI TETSUJI OTSUKI, HISASHI KOGA
PI TETSUJI OTSUKI, HISASHI KOGA
PI TETSUJI OTSUKI, HISASHI KOGA
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Primer fo
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1 (bases 1 to 2120)

Ota, T., Nishikawa, T., Isogai, T., Hayashi, K., Ishii, S., Kawai, Y., Wakamatsu, A., Sugiyama, T., Nagai, K., Kojima, S., Otsuki, T. and
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JP 2002017375-A/3289.
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Primer for synthesizing full-length cDNA and use thereof FH I
Location/Qualifiers
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                                                                                    GluPheLysTyrGlyAspLeuLeuGlyHisLeuLysIleMetHisAspAlaIleGlyPhe 80
                                                                                                                                 ATCCCAGTTATGGAGGGTGATGATGACACTGAAGTTTTTCGATTACAAGCCCCAGTATGG
                                                                                                                                                                                                 CGTCCAAAACCTGATCCTTATTGTCAAGCTAAGTATACTTTCTGTCCAACTGGCTCACCT
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                    ArgSerThrLeuThrGlyLysAsnTyrThrMetGluTrpTyrGluLeuPheGlnLeuGly 100
                                                               GAATTTAAATATGGAGACCTCCTGGGACACTTGAAAATTATGCATGATGCCATTGGATTC
                                                                                                                                                  | IleProValMetGluGlyAspAspAspIleGluValPheArgLeuGlnAlaProValTrp
   07-JUL-2000 JP 2000253172
TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAYASHI, SHIZUKO
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Direct Submission
Submitted (25 MAR-2002) Takao Isogai, Helix Research Institute,
Submitted (25 MAR-2002) Takao Isogai, Helix Research Institute,
Genomics Laboratory, 1532-3 Yana, Kisarazu, Chiba 292:0812, Japan
(B-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3985)
(B-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3985)
                                                                                                                        Sugiyama, T., Suzuki, Y., Nagai, K., Sugano, S., Lamara, Y., Sugiyama, T., Saito, K., Yamamoto, J., Wakamatsu, A., Nakamura, Y., Kawai-Hio, Y., Saito, K., Yamamoto, J., Ono, T., Okano, K., Yoshikawa, Y., Kojima, S., Nagahari, K., Masuho, Y., Ono, T., Okano, K., Iwayanagi, T. and notsuka, S., Sasaki, N., Hattori, A., Okumura, K., Iwayanagi, T. and
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Ninomiya,K.
                                                                                         Unpublished
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                                                               2 (bases 1 to 2120)
[sogai,T. and Otsuki,T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AlaGluPheGlyAlaGluPheLysAsnIleGluThrAsnTyrThrArgIlePheLeuTyr
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                                                                                                                                                                                                                       Metazoa;
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Primates;
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Catarrhini; Hominidae;
                                                                                                                                                                   ., Hayashi,K.,
K., Sugano,S.,
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Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction: Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center; cDNA 5'- & 3'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.).
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Secreted protein which human chromosome 13
Patent: UP 2001511345-A 12 14-AUG-2001;
ZYMOGENETICS INC
OS Artificial Sequence
PN JP 2001511345-A/12
PD 14-AUG-2001
PF 20-17UL-1998 JP 2000504249
PF 24-JUL-1997 US 60/053613
PR 24-JUL-1997 US 60/053613
PAUL O SHEEPPARD, DIBRA G GILBERTON
PC C12N15/09, A61K38/00, A61K48/00, C07K14/
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PAUL O SHEPPARD, DIBRA G GILBERTON
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                                                                                                                                             Mus musculus ceroid-lipofuscinosis, IMAGE:5251891), partial cds. BC025487 BC025487.1 GI:19343790
      Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
                                                                                                   Mus musculus
                                                                       Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                  Mus musculus
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                                                     nmalia; Eutheria; (bases 1 to 2318)
                                                                                                                  (house mouse)
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                                                                       Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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MEDLINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LLML at: http://lmage.llnl.gov Series: IRAK Plate: 56 Row: c Column: 7
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Web Site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Alkhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,B., Kwong,P., Laric,P., Legaspi,R.,
Hansen,N., Ho,S.-L., Karlins,B., Kwong,P., Laric,P.,
McCloskey,J.C.,
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphr, cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (06-MAR-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
22388257
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zhang, L.-H. and Green, E.D.
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/clone="IMAGE:5251891"
                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                               WAP-TGF alpha model.
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/db_xref="GI:19343791"
/db_xref="LocusID:211286"
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translation="TRPAHWRPALALALLGLATILGASPTSGQRWPVPYKRFSFRPKT/
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CLGIN	
ignment Scores: 1.12e-135 Length: 2318 red. No.: 1.423.00 Matches: 246 scrent Similarity: 89.03% Conservative: 30 sst Local Similarity: 79.35% Mismatches: 34 sery Match: 80.94% Indels: 0 s: 10 Gaps: 0	
3-10-010-050A-2_COPY_31_346 (1-316) x BC025487 (1-2318)	
7 SerArgArgHisTrpProValProTyrLysArgPheAspPheArgProLysProAspPro 26	0
27 TyrCysGlnAlaLysTyrThrPheCysProThrGlySerProIleProValMetGluGly 46	0
47 ASDASDASDILEGIUVAIPheArgLeuGInAlaProValTrpGluPheLysTyrGlyAsp 66 :::	0
67 LeuLeuGlyHisLeuLysIleMetHisAspAlaIleGlyPheArgSerThrLeuThrGly 86	0
87 LysaenTyrThrMetGluTrpTyrGluLeuPheGlnLeuGlyAsnCysThrPheProHis 10	30
107 LeuArgProGluMetAspAlaProPheTrpCysAsnGlnGlyAlaAlaCysPhePheGlu 12 381 CTCCGGCCTGACAAGAGCGCTCCCTTCTGGTGTAACCAAGGGGCAGCCTGCTTTTTTGAA 44	9 8
127 GlyIleaspäspvalhistyplysgluäsnglythyleuvalglnvalälathyilesey 14	0 6
147 GlyagnMetpheAsnGlnMetAlaLysTrpValLysGlnAspAsnGluThrGlyIleTyr 16	0 6
167 TyrGluThrTrpAsnValLysAlaSerProGluLysGlyAlaGluThrTrpPheAspSer 18	ဝ ရ
187 TyraspCysSerLysbheValleuargThrPheAsnLysLeualaGluPheGlyAlaGlu 20	5 6
207 PheLybasnileGluThrasnTyrThrargilePheLeuTyrSerGlyGluProThrTyr 22	90
9 227 LeuGlyAsnGluThrSerValDheGlyProThrGlyAsnLySThrLeuGlyLeuAlaIle 24 	00 6
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Yoon, V.,

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Malen, C., Alden, H., Alsbrooke, S., Amin, A., Angulanto, D., Alder, J., Allen, C., Allen, H., Alsbrooke, S., Amin, A., Angulanto, D., Allen, C., Allen, H., Alsbrooke, S., Amin, A., Angulanto, D., Anylebechi, V., Ayodej, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benalmed, F., Eiswalo, K., Blair, J., Blankenburg, K., Casasr, H., Center, A., Chacko, J., Chacko, J., Chacko, J., Cher, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Cheveland, C., Cockeell, R., Cox, C., Coyle, M., Cree, A., pr. Souza, L., Davila, M. L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Davigado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Digan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Beootto, M., Engene, C., Evans, C.A., Falls, T., Fan, G., Franser, C.M., Gabsia, A., Ganta, R., Garcia, M., Marcia, M., Garcia, M
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AC109554.4 GI:23820683
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On Oct 11, 2002 this sequence version replaced gi:21738217.
On Oct 11, 2002 this sequence version replaced gi:21738217.
On Oct 11, 2002 this sequence version replaced gi:21738217.
On Oct 11, 2002 this sequence version replaced gi:21738217.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgcc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature
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Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NOTE: Betimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

This sequence will be replaced by the finished sequence as soon as it is available and the sequence as soon as it is available and the sequence as soon as it is available and the sequence as soon as it is available and the sequence as soon as it is available.
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1 198524: contig of 198524 bp
Location/Qualifiers
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Center clone name: GQLY
Center clone name: CH230-331D3
Center clone name: CH230-331D3
Assembly program: Phrap; version 0.990329
Consensus quality: 177481 bases at least Q40
Consensus quality: 179480 bases at least Q30
Consensus quality: 181141 bases at least Q30
Consensus quality: 181141 bases at least Q30
Consensus quality: 181141 bases at least Q30
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/note="clone_boundary
clone_end:T7
                                                                          site:MboI
                                                                                                                                                                                                                                                                                                                                                                /organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
                                     end_sequence:RXAPC14TJ"
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:-10-010-050A-2_COPY_31_346 (1-316) x AC109554 (1-198524)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGAAACACGTTTAACAAAGTGGCCGAGTGGGTGAAGCAGGACAATGAGACTGGGATTTAT 38078
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGAATTTACGATAAACACTGGAAGGAAAACGGGACGTTGTCTCTGGTTGCAACCATATCC 38.38
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                                                                                                                                                        LygArgPheTyrTyrProPheLygProHisLeuProThrLygGluPheLeuLeuSerLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  TACGACTGTTCGAATTTTGTCTTAAGGACATATGAGAAATTGGCTGAATTTGGAACAGAA 37958
TTGAAAATTTTTGACACAGTGATTATGCACAGAGAGTTCTACCTGTTTTATAACTTTGAG 37/18
                                                 LeuGlnIlePheAspAlaValIleValHisLysGlnPheTyrLeuPheTyrAsnPheGlu
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                                        MILEN, M., MELLE, M., MELEN, M., MAILEN, M., MAILEN, M., MAILEN, M., MECA, B., Maden, H., Alsbrooks, S., Malin, R., Angulano, D., Anayalebechi, V., Aoyagi, A., Ayodeji, M., Baca, B., Maden, H., Balwan, D., Bandarananake, D., Barber, M., Barnstead, M., Benahmed, F., Balwan, D., Bandarananake, D., Barber, M., Barnstead, M., Benahmed, F., Balwan, D., Bandarananake, D., Barber, M., Barnstead, M., Benahmed, F., Balwan, D., Bandarananake, D., Chen, Y., Calderon, E., Chu, J., Chacko, J., Chacko, J., Chacko, J., Chacko, J., Chacko, J., Cardenas, W., Carter, K., Cavazos, I., Ceasar, H., Center, A., D'Souza, L., Cardenas, W., Carter, K., Cavazos, I., Ceasar, H., Canter, A., D'Souza, L., Davila, M., Dagnar, R., Davila, M., Duval, B., Eaves, K., Egan, A., Escotto, M., Ebgen, C., Swans, C.A., Falls, T., Fan, G., Chen, Y., Chen, Z., Chu, J., Chen, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Praser, C.M., Gabisia, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Genraet, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, K., Genraet, P., Haland, S., Hadun, S.L., Hodgson, A., Hogues, M., Hernandez, J., Harles, S., Hadun, S.L., Hodgson, A., Hogues, M., Hernardez, R., Hines, S., Hadun, S.L., Hodgson, A., Hogues, M., Hernardez, J., Loulas, B., Howells, S., Huyk, S., Hung, L., Kowar, C., Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kowar, C., Kows, S.C., Kraft, C.L., Lebow, H., Lozado, R.J., Lowison, A., Joixet, A., Kows, C., Kraft, C.L., Lebow, H., Lozado, R.J., Lowison, A., Joysen, A., Mangum, B., Mahindartne, M., Mahmoud, M., Malloy, K., Manyum, A., Manhamartne, M., Mahmoud, M., Malloy, K., Manyum, A., Mangum, B., Mahindartne, M., Mahmoud, M., Malloy, K., Manyum, A., Manhamartne, M., Mahmoud, M., Malloy, K., Manyum, A., Manhamartne, M., Mahmoud, M., Malloy, K., Martin, R., Martin, S., Patks, K., Maynum, A., Mayn
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Rattus norvegicus clone CH230-138J6, *** SEQUENCING IN PROGRESS
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                   No.:
                                                                                                                                                        misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (23-JAN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (13-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On May 13, 2003 this sequence version replaced gi:22855855. The sequence in this assembly is a combination of BAC based reads The sequence in this assembly is a combination of BAC based reads.
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Rat Genome Sequencing Consortium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NOTE: Estimated insert size may differ from sequence length (see http://www.bgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
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Center clone name: CH230-138J6
Center clone name: CH230-138J6
Center clone name: CH230-138J6
Center clone name: CH230-138J6
Assembly program: Atlas 3.0;
Consensus quality: 214528 bases at least Q40
Consensus quality: 217333 bases at least Q20
Consensus quality: 219034 bases at least Q20
Estimated insert size: 223690; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
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223660
224739
224839
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226390
                                                                                       /note="wgs_contig"
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/note="wgs_contig"
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                                                                                                                                                                               /mol_type="genomic DNA"
/db_xref="taxon:10116"
/clone="CH230-138J6"
                                                                                                                                                                                                                                         organism="Rattus norvegicus"
1.7e-124
1339.00
                                                                                                                                                                                                                                                                                                     223559: contig of 223559 bp in length
223659: gap of unknown length
224738: contig of 1079 bp in length
224838: gap of unknown length
226289: contig of 1451 bp in length
226389: gap of unknown length
226389: gap of unknown length
227920: contig of 1531 bp in length
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Direct Submission
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32214 CTGTTGAGTCTCTTGCAAATTTTTGATGCAGTGATTGTGCACAAACAGTTCTATTTGTTT
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Assembly program: XGAP4; version 4.5
Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08755; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 162085 bases at least Q40
Consensus quality: 164521 bases at least Q30
Consensus quality: 164521 bases at least Q20
Consensus quality: 166040 bases at least Q20
Insert size: 168062; sum-of-contigs
Insert size: 164996; 1.7% error; agarose-fp
Quality coverage: 4.08x in Q20 bases; sum-of-contigs Quality
coverage: 4.16x in Q20 bases; agarose-fp
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Center code: SC
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HTG; HTGS_PHASE1; HTGS_CANCELLED
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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----- Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Web site: http://www.sanger.ac.uk
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NOTE: This is a 'working draft' sequence. It currently consists of 14 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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165025: contig of 7689 bp in
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                            Homo sapiens chromosome 13 clone
AL359875
AL359875.3 GI:9864226
HTG; HTGS_PHASE1; HTGS_CANCELLED.
Homo sapiens (human)
        Direct Submission
Submitted (12-JUN-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk
                                                                                           Burton, J
                                                                                                                                                                             Homo sapiens
                                                                                                                                                     Eukaryota;
                                                                                                                                                                                                                                                                                                     AL359875
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GluProThrTyrLeuGlyAsnGluThrSerValPheGlyProThrGlyAsnLysThrLeu 242
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fragment_chain:2
clone_end:SP6
vector_side:right"
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Eutheria;
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89.69%
89.18%
52.65%
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chromosome 13 clone
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Primates;
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142

ATURES source

misc

HTG

13-JUN-2001

302

118717 282 118657

misc

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MMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Insert size: 245987; sum-of-contigs
Insert size: 190986; agarose-fp
Quality coverage: 2.52x in Q20 bases; sum-of-contigs Quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Assembly program: XGAP4; version 4.5 sequencing vector: plasmid; L08752; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Consensus quality: 220597 bases at least Q40 Consensus quality: 234299 bases at least Q30 Consensus quality: 241103 bases at least Q20 Consensus quality: 241103 bases at least Q20
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Center code: Si
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          coverage: 3.92x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Web site: http://www.sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                    NOTE: This is a 'working draft' sequence. It currently consists of 53 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
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GAACCTACTTATCTGGGAAATGAAACATCTGTTTTTGGGCCAACAGGAAAACAAGACTCTT
              GluProThrTyrLeuGlyAsnGluThrSerValPheGlyProThrGlyAsnLysThrLeu 242
                                                                          PheGlyAlaGluPheLysAsnIleGluThrAsnTyrThrArgIlePheLeuTyrSerGly
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                                                                                                                                                                 <u>ACAGGAATTTATTATGAGACATGGAATGTAAAAGCCCAGCCCAGAAAAGGGGGGCAGAGACA</u>
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Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y., Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and
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                                           ArgValSerGlyIleProSerArgArgHisTrpProValProTyrLysArgPheAspPhe
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mer for synthesizing full-length cDNA and use thereof FH Key
Location/Qualifiers
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TOSHIO OTA,TETSUO NISHIKAWA,TAKAO ISOGAI,KOJI HAYASHI,SHIZUKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Conservative:
Mismatches:
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Gaps:
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Homo sapiens (human)
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1 (beg) 1 to 697)
Ota, T., Nishikawa, T., Tsogai, T., Hayashi, K., Ishii, S., Kawai, Y., Wakamatsu, A., Sugiyama, T., Nagai, K., Kojima, S., Otsuki, T. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BD126453.1 GI:23221398 JP 2002017375-A/1884.
                                                                                                                                                                                                                                                                                             Primer for synthesizing full-length cDNA and use thereof Patent: JP 2002017375-A 1884 22-JAN-2002;
HELIX RESEARCH INSTITUTE
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                                                                              C12P21/02,C12Q1/68//C12P21/08,G06F17/30,C12N15/00,C12N5/00
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                                                                                                                                                          TETSUJI OTSUKI, HISASHI KOGA
                                                                                                                                                                                      YURI KAWAI,AI WAKAMATSU,TOMOYASU SUGIYAMA,KEIICHI NAGAI,
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07-JUL-2000 JP 2000253172
TOSHIO OTA,TETSUO NISHIKAWA,TAKAO ISOGAI,KOJI HAYASHI,SHIZUKO
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JP 2002017375-A/1884
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/organism='Homo sapiens (human)'
Location/Qualifiers
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                                                               r synthesizing full-length cDNA and use thereof Location/Qualifiers
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                Eukaryota;
                           Mus musculus
                                             Mus musculus (house mouse)
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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The strings of n's in this record represent gaps between contigs, and the length of each string corresponds to the length of the gap except where there are 20 n's. A string of 20 n's represents a gap of unknown length.
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Peterson,K., King,B., Hagge-Greenberg,A., Roix,J., Bult,C. and
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66916. .>68607)
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IIKRHSNHLQYVSFKVDSSKESAEAACDILSQLVNCSLKTLGLISTARPSFMDLPKSH
FISALTVVFVNSKSLSSLKLDDFPVDDPSLKVLVANNSDTLKLLKMSSCPHVSBAGIL
CVADQCHGLRELALNYHLLSDELLLALSSEKHVRLEHLRIDVVSENPGGTHFHTIQKS
SWDAFIKHSPKVNLVMYFFLYBEEFDPFFRYEIPATHLYFGR8VSKDVLGRVGMTCPR
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/product="immuneoresponsive gene 1"
/product="immuneoresponsive gene 1"
/note="partial transcript sequence derived from
to GenBank Accession Number L38281"
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complement (<73858. .>86476)
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/gene="Fbl3a"
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complement(<106136...>339446)
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/note="partial transcript derived from alignment
tentative consensus sequence TC227789, from TIGR
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/note="PAM, protein associated with Myc; partial transcript derived from alignment of Homo sapien: RefSeq sequence NM_015057"
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                                                                                                                        LeuGlnIlePheAspAlaValIleValHisLysGlnPheTyrLeuPheTyrAsnPheGlu 286
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CCTACCCGACATACAACATTTACCGACTTG
                                                  TATTGGTTTCTACCAATGAAACCCCCCTTTGTCAAAATAACATACGAAGAAACCCCCGTTA 67394
                     ProlleArgAsnLysThrLeuSerGlyLeu 316
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Search completed: April 25, 2004, 03:23:00 Job time : 6261.28 secs

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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OS Homo sapiens (human)
PN JP 2002017375-A/618
PD 22-JAN-2002
PD 22-JAN-2002
PF 07-JUL-2000 JP 200025:
PI TOSHIO OTA, TETSUO NIS)
PI ISHII,
PI YURI KAWAI, AI WAKAMAT
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Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 697)
Ota, T., Nishikawa, T., Isogai, T., Hayashi, K., Ishii, S., Kawai, Y., Wakamatsu, A., Sugiyama, T., Nagai, K., Kojima, S., Otsuki, T. and
                                                                                       Homo sapiens
                                                                                                                               BD126453.1 GI:23221398 JP 2002017375-A/1884.
                                                                                                                                                                    BD126453
                                                                                                          Homo sapiens (human)
                                                                                                                                                                                                        BD126453
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mer for synthesizing full-length cDNA and use thereof FH K
Location/Qualifiers
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07-JUL-2000 JP 2000253172
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                                                                                                                                                                                 for synthesizing full-length cDNA and use thereof
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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S., Otsuki,T. and
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Roga, H.

Primer for synthesizing full-length cDNA and use thereof

Patent: JP 2002017375-A 1884 22-JAN-2002;

HELIX RESEARCH INSTITUTE
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PI TETSUJI OTS
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1 (bases 1 to 1486)
Sheppard, P.O. and Gilberton, D.G.
Secreted protein which human chromosome 13 encodes
Patent: JP 2001511345-A 1 14-AUG-2001;
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Secreted protein which human chromosome 13
ED073402
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C12N1/21,C12N5/10,C12P21/02,C12Q1/68,C12N15/00,A61K37/02,C12N5/
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TOSHIO OTA,TETSUO NISHIKAWA,TAKAO ISOGAI,KOJI HAYASHI,SHIZUKO
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                                                                                         14-AUG-2001
24-UL-1998 JP 2000504249
24-UL-1997 US 60/053613
24-UL-1997 US 60/053613
PAUL O SHEPPARD, DIBRA G GILBERTON
PAUL O SHEPPARD, DIBRA G GILBERTON
C12N15/09, A61K38/00, A61K48/00, C07K14/47, C07K16/18, C12N1/15,
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Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Indels:
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st Local Similarity:
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PN JP 2002506627-A/25

PD 05-MAR-2002

PF 18-MAR-1999 UP 2000536733

PF 18-MAR-1998 US 60/078566,19-MAR-1998 US

19-MAR-1998 US 60/078573,19-MAR-1998 US

19-MAR-1998 US 60/078579,19-MAR-1998 US

19-MAR-1998 US 60/078579,19-MAR-1998 US

19-MAR-1998 US 60/078579,19-MAR-1998 US

19-MAR-1998 US 60/078579,19-MAR-1998 US

19-MAR-1998 US 60/078563,01-APR-1998 US

01-APR-1998 US 60/078563,01-APR-1998 US

01-APR-1998 US 60/078579,01-APR-1998 US
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PI DANIEL R SOPPET, YING FEI WEI, GREGORY A ENDRESS, ROXANNE D DUAN,
PI HLA KYAW,
PI KEINHARD EBNER, DAVID W LAFLEUR, HENRIK S OLSEN, YANGGU SHI, PAUL,
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PI A MOORE
PC C12N15/09, A61K38/00, A61K48/00, A61P43/00, C07K14/47, C07K16/18,
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Patent: JP 2002506627-A 25 05-MAR-2002;
HUMAN GENOME SCIENCES INC
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Ruben,S.M., Ni,J., Rosen,C.A., Yu,G.L., Young,P.B., Fen,P.
Soppet,D.R., Wei,Y.F., Endress,G.A., Duan,R.D., Kyaw,H., E
Lafleur,D.W., Olsen,H.S., Shi,Y. and Moore,P.A.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Primer for synthesizing full-length cDNA and use thereof Patent: JP 2002017375-A 3289 22-JAN-2002;

HELIX RESBARCH INSTITUTE
OS Homo sapiens (human)
P 002017375-A/3289
PD 22-JAN-2002
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1 (bases 1 to 2120)

Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y., Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and
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ner for synthesizing full-length cDNA and use thereof FH F
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TOSHIO OTA,TETSUO NISHIKAWA,TAKAO ISOGAI,KOJI HAYASHI,SHIZUKO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (255 MAR-2002) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) NEDO human cDNA sequencing project supported by Ministry of NEDO normy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction: Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center; cDNA 5'- & 3'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.).
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Isogai,T. and Otsuki,T.
Direct Submission
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sapiens (human)
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/clone_lib="plaCE1"
/note="cloning vector: I
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/mol_type="mRNA"
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Savukoski, M., Klockars, T.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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IDDVHHKENGTLVQVATISGNMFNQMAKWVKQDNETGIYYETWNVKASPEKGAETWFD
SYDCSKFVLRTFNKLAEFGAEFKNIETNYTRIFLYSGEPTYLGNETSVEGETGNKTLG
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AC001226.1 GI:2133862
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Submitted (29-MAY-1997) Whitehead Institute/MIT Center for Genome Submitted (29-MAY-1997) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA on May 29, 1997 this sequence version replaced gi:1932720. The Staden databases, finishing information, and all chromatographic files used in the assembly of this clone are available from our anonymous ftp site.
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Hawkins, T.L., Reeve, M.P., Chrasman, K.H. and Lander, E.S.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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http://ftp.genome.washington.edu/RM/RepeatMasker.html
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3552. .3828
/rpt_family="AluJb"
4361. .4640
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complement(11471. .11495)
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complement(12394. .12440)
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/rpt_family="AT_rich"
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/rpt family="GC rich"
complement (23546. .23578)
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24565. .24707
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21238.
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/rpt_family="FAM"
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/rpt family="AT rich"
complement (47411. .47431)
/rpt family="AT rich"
complement (47612. .47684)
/rpt_family="(CATA)n"
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complement(40741. .4091=1
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/rpt_family="AT_rich"
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/rpt_family="MIR"
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complement(54755. .54782)
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/rpt family="AluJo"
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Homo sapiens chromosome 13 clone RP11-185124, 14 unordered pieces.
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HTG; HTGS_PHASE1; HTGS_CANCELLED
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Contact: humquery@sanger.ac.uk
------ Project Information
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On Sep 8, 2000 this sequence version replaced gi:6982057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (10-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AL136440
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center project name: bA185124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center code: SC
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                                                                                                                                                                                                                                                                                                                                                      arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                   NOTE: This is a 'working draft' sequence. It currently consists of 14 contigs. The true order of the pieces is not known and their order in this sequence record is
                 3401
3501
16445
19545
19615
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19615
22242
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25527
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33171
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3500: gap of
16444: contig
16544: gap of
19514: contig
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contig
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If 100 bp

of 2627 bp in length

of 100 bp

g of 3185 bp in length
                   of 34450 bp in length
100 bp
of 25693 bp in length
                                                                                                                                                                                                                                                                                                  100 bp
of 12944 bp in length
100 bp
                                                                                                                                                                                                                                                                                                                                             of 3400 bp in length
                                                                                                                                                                                        100 bp
of 7444 bp in length
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in length ij in length length

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lest Local Similarity:
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fragment_chain:1"
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fragment_chain:1"
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mol_type="genomic DNA"
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147236: gap of 100 bp
164925: contig of 17689 bp in length
165025: gap of 100 bp
169362: contig of 4337 bp in length.
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AL359875
AL359875.3 G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
-----Project Information
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Insert size: 245987; sum-of-contigs
Insert size: 190986; agarose-fp
Quality coverage: 2.52x in Q20 bases; sum-of-contigs Quality
coverage: 3.92x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (12-JUN-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
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Mammalia; Eutheria;
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Primates;
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85667: 85567: 68040: 75029:

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gap of 100 bp
contrig of 6989 bp in length
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11 234942: contig of 2232 bp in length
13 235042: gap of 100 bp
13 240558: contig of 5916 bp in length
15 241058: gap of 100 bp
19 251187: contig of 10129 bp in length.
1 Location/Qualifiers
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/note="assembly_fragment:00352
fragment_chain:1"
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/note="assembly_fragment:00920
fragment_chain:4"
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/note="assembly_fragment:01277
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="13"
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/note="assembly_fragment:00448
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/note="assembly fragment:00009
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fragment_chain:4"
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OS Artificial SS
PN JP 201511349
PD 14-AUG-2001
PF 24-JUL-1998
PR 24-JUL-1997
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PG C12N15/09,A6
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BD073413.1 GI:22619016
JP 2001511345-A/12.
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AL672113 AL672111
AL672113.1 GI:20803952
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1 (bases 1 to 152050)
Sullivan, J.T., Trzebiatowski, J.R., Cruickshank, R.W., Gouzy, J.,
                        Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Phyllobacteriaceae; Mesorhizobium.
                                                            Mesorhizobium loti
                                                                           Mesorhizobium loti
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              (bases 1 to 152050)
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24-JUL-1997 US 66/053613
PAUL O SHEPPARD, DIBRA G GILBERTON
C12N15/09, A61K38/00, A61K48/00, C07K14/47, C07K16/18, C12N1/15,
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mesorhizobium Toti strain R7A
J. Bacteriol. 184 (11), 3086-3095 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Comparative sequence analysis of the symbiosis island of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and Ronson, C.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Brown, S.D., Elliot, R.M., Fleetwood, D.J., McCallum, N.G. Rosebach, U., Stuart, G.S., Weaver, J.E., Webby, R.J., de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (07-FEB-2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ronson, C.W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /protein id="CAD31530.1"
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/gene="nolo"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gene name confidence : putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement (104. .2125)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="PROBABLE TRANSFERASE, NODULATION PROTEIN NOLO"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         B
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YLFGI.GTGI.GIMVGRVDGASYIAFLAAGMVAVSAMTASTLETI.YAAFARMHSQRTWEA
MLYTHITLGDIVLGELAWAATKAFWAGTAITIVTATLGYAAWPSVLYALPIIALTGCV
FASLAMIVTALSPSYDYFVFYQTLVLTPMLFLSGAVFPLNQLPGAFQQIARCMPLSHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gene name confidence : putative"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EGEAVLADLLDTITLDQAQREALTGELRRLWEQRRVRMRPSQAARVDQN"
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/note="Product confidence : probable
                                                                                                                                                                                                                                                                                                                                                                  transl table=1
                                                                                                                                                                                                                                                                                                                                                                                                    evidence=not_experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                   codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                confidence : probable
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GEPWPSVDVIIPCYNEAPRTLSDCLASIASQEYAGKLQVYVUDGSANRDALVGVHEE
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QMTACLMIAAMTIVRCSVAAFFARQLRFLGFSLHTLINIFLLLPLKAYALCTLSN3DW
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N-ACETYLGLICOSAMINYLTRANSFERASE"
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/note="Product confidence : probable
Gene name confidence : putative"
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AHSISVMYPVLQQLGVPFAFGTVRQALRNHVSRFCRKGLANILTGVRVRSTLPDVYSD
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/note="Product confidence : probable
Gene name confidence : putative"
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                                                                         /gene="msil30"
6579. .6833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement (5624. .6220)
/gene="nodA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement (5624. .6220)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LSRSSAANVTDTGGTSSKPNLVGSDAAYSEQQ"
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'note="Product confidence : probable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'gene="nodI"
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  hypothetical
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US-10-010-050A-2_COPY_1_28 (1-28) x ML0672113 (1-152050)
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DB:
                                                                                                     SOURCE ORGANISM
                                                                                                                                                                                                                                                      HSBA19D2/c
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
                                       REFERENCE
                                                                                                                                                                                                                              DEFINITION
                                                                                                                                                                                                                                                                                           RESULT 13
                                                                                                                                            KEYWORDS
                                                                                                                                                                  VERSION
                                                                                                                                                                                      ACCESSION
AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       No.:
                                                                                                                                                                                                                                                                                                                                     130027 ATGCAAACAGGAGCCGGAAGGTGTCGCGGTAGGAGGCGATGGTGTTGGAGCTTACGCCTC 129968
                                                                                                                                                                                                                                                                                                                                                               1 MetArgArgGlyAlaGlyAlaAlaArgGlyArgAlaSerTrpCysTrpAlaLeuAlaLeu 20
                                                                                                                                                                                                     Human DNA sequence from clone RP11-19D2 on a putative novel gene, ESTs, STSs and GSSs,
                                                                                                                                                                                        a putative
AL080248
  Direct Submission
                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                        HSBA19D2
                     McMurray, A.
                                                                                                                             Homo sapiens (human)
                                                                                                                                                                    AL080248.7 GI:5725257
                                       (bases 1 to 166913)
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/note="Product confidence : probable
Gene name confidence : putative"
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/gene="nods"
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GEREGARPDGATSNELFEVLADWNTQLEHLRPEVRKGAGP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /function="small molecule metabolism"
/note="Product confidence : putative
Gene name confidence : hypothetical"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gene name confidence : hypothetical"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement (8659. .9840)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  METHYLTRANSFERASE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
/evidence=not_experimental
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement (7450. .8058)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="HYPOTHETICAL PROTEIN"
/protein_id="CAD31535.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement (8659. .9840)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="GI:20803958"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'evidence=not_experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 product="pUTATIVE OXIDOREDUCTASE PROTEIN"
(protein id="CAD31537.1"
/db_xref="G1:20803960"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="msil32"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="PROBABLE NODULATION PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene="nods"
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60.00%
47.40%
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                                                                                                                                                                                                                                    RP11-19D2 on chromosome 20. Contains
                                                                                                                                                                                                                                                          DNA
                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                     complete sequence.
                                                                                                                                                                                                                                                            PRI 10-MAR-2001
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<pre>variation /replace="gcc" /replace="gcc" 932934 /note="clone Rp5-988G17 tat in this entry substitution" /replace="ttt" /replace="ttt" /replace="ttt" /note="MSTA repeat: matches 1426 of consensus" variation /note="clone Rp5-988G17 gct in this entry substitution" /replace="gat"</pre>	variation Just 1997 variation /note="clone RP5-988G17 zaa in this entry substitution" /replace="ata" variation /note="clone RP5-988G17 tat in this entry substitution" /replace="tgt" /replace="tgt" /note="clone RP5-988G17 fote in this entry yariation /note="clone RP5-988G17 fote in this entry gtc in this entry	numbers given in the feature table with their source databases: Em: EMBL; Sw: SWISSPROT; Tr: TREMBL; Wp: WORNPEP; Information on the WORNEPP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 20, constructed by the Sanger Centre Chromosome 20 Mapping Group. Further information can be found at http://www.sanger.ac.uk/PROP/Chr20 Mapping Group. Further information can be found at http://www.sanger.ac.uk/PROP/Chr20 Mis sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 10; an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. RP11-19D2 is from the library RPCI-11.1 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm VECTOR: pBACe3.6 IMPORTANT: This sequence is not the entire insert of clone RP11-19D2 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap. The true right end of clone RP11-19D2 is at 1 in this sequence. Location/Qualifiers source // clone lib="RPCI-11.1" misc_feature 8277 // clone lib="RPCI-11.1" misc_feature 8277 // clone lib="match: STS: Em:G48897 match: SSS: Em:B81947" 105. 107 105. 107 107. 107 107. 107 107. 107 107. 107 107. 107 107. 107 107. 107 107. 107 107. 107 107 107 107 107 107 107 107	JOURNAL Submitted (02-MAR-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk MMENT On Aug 10, 1999 this sequence version replaced gi:5596948. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
region /note=" region 1845a region 19091. region 19091. /note=" eature /note=" eature /note=" fon 20104. /note=" ion 20304. /note=" agt in substit	tches 47933 tches 53315 tches 35084 atches 1913 atches 5894 atches 1307	on region	

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RESULT 14
AC079116/c
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Best Local Similarity:
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VERSION
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                                                                                                                                                                                                                                                                      156588 TGCAGGGTA 156580
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                                                                                                                                         147856 bp DNA linear HTG 23-SEP-2000
Homo sapiens chromosome UNK clone RP11-103D9, WORKING DRAFT
SEQUENCE, 9 unordered pieces.
ACO79116
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 147856)
                                                          Homo sapiens
                                                                          Homo sapiens (human)
                                                                                          HTG; HTGS_PHASE1; HTGS_DRAFT
                                                                                                                 AC079116.2 GI:10280934
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/note="MERTA repeat: matches 2..346 of consensus"
/note="Match: STS: Em:Z5207,78259. .78297))
/note="match: STS: Em:Z52394"
/join(25143. .25339,82904. .82972)
/note="match: STS: Em:G07821"
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/note="match: GSS: Em:AL023755"
complement(join(24573. .24708,82902. .82963))
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23244. .23380
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20823. .21222
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25935. .25937
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23350. .23352
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24007. .24009
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The sequence of Homo sapiens clone unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (18-AUG-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA On Sep 23, 2000 this sequence version replaced gi:9845173.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 (bases 1 to 147856)
Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequencing vector: plasmid; 0% Chemistry: Dye-primer ET; 100% of reads Chemistry: Dye-terminator Big Dye; 0% of reads Assembly program: Phrap; version 0.990319 Consensus quality: 142405 bases at least Q40 Consensus quality: 144423 bases at least Q20 Consensus quality: 145315 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center project name: H_NH0103D09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center code: WUGSC
Web site:http://genome.wustl.edu/gsc/index.shtml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center: Washington University Genome Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Quality coverage: 5.04 in Q20 bases; agarose-fp
Quality coverage: 5.59 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Insert sizē: 162000; agarose-fp
Insert size: 146912; sum-of-contigs
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112403
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1832
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                                                                                      vector_side:left"
                                                                                                        clone_end:SP6
                                                                                                                           /note="assembly_name:Contig46
                                                                                                                                                               /note="assembly_name:Contig45"
                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                    organism="Homo sapiens"
                note="assembly_name:Contig47"
                                                  note="assembly_name:Contig14"
                                                                                                                                                                                                         clone="RP11-103D9"
                                                                                                                                                                                                                              db_xref="taxon:9606"
chromosome="UNK"
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                                                                                                                                                                                                                                                                                                                                             112402: contig of 33832 bp in 112502: gap of unknown length 147856: contig of 35354 bp in
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10519: contig of 7288 bp in length
10619: gap of unknown length
27623: contig of 17004 bp in length
277723: gap of unknown length
                                                                                                                                                                                                                                                                  type="genomic
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1831: gap of unknown length
2887: contig of 1056 bp in length
2987: gap of unknown length
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of 26839 bp in length
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                                                                                                                                                  Waterston,R.H.
Direct Submission
Submitted (15-JUL-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
MO 63108, USA
5 (bases 1 to 152996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mammalia; Eutheria; Primates; 1 (bases 1 to 152996) Sulston, J.E. and Waterston, R.
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AC008177.3
                                                                Submitted (07-OCT-2000) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 6 (bases 1 to 152996)
                                                                                                                                                                                                                                                                                                                                                                                                              Edwards, J., Maupin, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Toward a complete human genome sequence Genome Res. 8 (11), 1097-1108 (1998)
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Direct Submission
Submitted (25-MAR-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
                                                                                                                                  5 (bases 1 to 152996) Waterston, R.
                                                                                                                                                                                                                                                                                        Submitted (28-JUL-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                                                                                                                                                                                                                                                                                                                                          Waterston, R.H.
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Unpublished (2001)
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112503. .147856
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Eutheria; Primates;
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REFERENCE
AUTHORS
TITLE
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                                                                                                                                                                               JOURNAL
                                                                                                                   Submitted (29-OCT-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, on Oct 7, 2000 this sequence version replaced gi:9211468.
                                                                                                                                                                                                                  7 (bases 1 to Waterston, R.
                                                                                                                                                                                                                                             MO 63108,
7 (bases
                                                                                                                                                                                                      Direct Submission
Center project name: H_NH0527A07
                    Contact: sapiens@watson.wustl.edu
                                                                              Center: Washington University Genome Sequencing Center Center code: WUGSC
                                                           Web site: http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                               USA
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING IMPORMATION:
Mapping information for this clone was provided by Dr. John D.
Mapping information for Genetics, Washington University, St. Louis
McPherson, Department of Genetics, Washington University, St. Louis
McPherson, Importantion about the map position of this
MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc

donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at http://www.chori.org The RPCI-11 human BAC library was made from the blood of SOURCE INFORMATION: pBACe3.6 one male

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the right is RP11-18C9, 200 base pair overlap. Actual start of this clone is at base position 1 of RP11-527A7, actual end is at base position 42119 of RP11-18C9

FEATURES repeat_region repeat_region repeat_region repeat_region source repeat_region repeat_region repeat_region /rpt_family="L2" 7932..8185 Location/Qualifiers 'rpt_family="MER2_type" clone="RP11-527A7" clone_lib="RPCI-11" 'mol_type="genomic DN 'db_xref="taxon:9606" chromosome="2" organism="Homo sapiens" rpt_family="L1" rpt_family="MER2_type" map="2" .152996 _family="L1" _family="L1" family="MIR' .2830 6107 DNA"

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31862. .32102
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Percent Similarity:
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Search completed: April 25, 2004, 03:24:31 Job time : 620.278 secs
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39528. .39830
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39982. .40376
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41336. .41487
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42204. .42336
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Dmmand line parameters:
MODEL=frame+ p2n.model -DEV=xlh
P2=/cgn2 1/USPTO spool/US10010050/runat 22042004_113204_27549/app_query.fasta_1.1372
PB=/cgn2 1/USPTO spool/US101-1--MATRIX=D10sum62 -TRANS=human40.cdi -LIST=45
DCALIGN=200 -THR SCORE=pct -THR MAX=100 -TRA MIN=0 -ALIGN=15 -MODE=LOCAL
DUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
TSER=US10010050 @CGN 1 17433 @runat 22042004 113204 27549 -NCPU=6 -TCPU=3
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OS Homo sapiens (human)
PN JP 2002017375-A/618
PD 22-JAN-2002
PC 07-JUL-2000 JP 200025:
PI TOSHIO OTA, TETSUO NISI
PI ISHII,
PI YURI KAWAI, AI WAKAWAT.
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1 (bases 1 to 697)
Ota, T., Nishikawa, T., Isogai, T., Hayashi, K., Ishii, S., Kawai, Y., Wakamatsu, A., Sugiyama, T., Nagai, K., Kojima, S., Otsuki, T. and
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JP 2002017375-A/618.
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Patent: JP 2002017375-A 618 22-JAN-2002;
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Primer for synthesizing full-length cDNA and use thereof FH I
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 697) Ota, T., Nishikawa, T., Isogai, T., Hayashi, K., Ishii, S Wakamatsu, A., Sugiyama, T., Nagai, K., Kojima, S., Otsu
                                                                                                                                                    Homo sapiens (human)
Homo sapiens
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TOSHIO OTA,TETSUO NISHIKAWA,TAKAO ISOGAI,KOJI HAYASHI,SHIZUKO
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Primer for synthesizing full-length cDNA and use thereof
Patent: JP 2002017375-A 1884 22-JAN-2002;

HELIX RESEARCH INSTITUTE
OS Homo sapiens (human)
PN JP 2002017375-A/1884
PD 22-JAN-2002
PD 22-JAN-2002
PD 07-JUL-2000 JP 2000253172
PI TOSHIO OTA,TETSUO NISHIKAWA,TAKAO ISOGAI,KOJI HAYASHI,PI ISHI,
PI ISHI, VATAMA,AI WAKAMATSU,TOMOYASU SUGIYAMA,KEIICHI NAGA
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Primer for synthesizing full-length cDNA and use thereof FH K
Location/Qualifiers
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SHINICHI KOJIMA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37
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JP 2001511345-A/1
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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C12N1/21, C12N5/10, C12P21/02, C12Q1/68, C12N15/00, A61K37/02, C12N5/
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TOSHIO OTA,TETSUO NISHIKAWA,TAKAO ISOGAI,KOJI HAYASHI,SHIZUKO
                                                                                                                                                                                                                 Homo sapiens (human)
JP 2001511345-A/1
14-AUG-2001
                                                                                           24-JUL-1998 JP 2000504249
24-JUL-1997 US 60/053613
PAUL O SHEPPARD, DIBRA G GILBERTON
C12N15/09, A61K38/00, A61K48/00, C07K14/47, C07K16/18, C12N1/15,
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/mol_type="genomic DNA"
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95 human secretory proteins.
BD136338
BD136338.1 GI:23231283
JP 2002506627-A/25.
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1 (bases 1 to 1751)

Ruben,S.M., Ni,J., Rosen,C.A., Yu,G.L., Young,P.E., Fen,P., Soppet,D.R., Wei,Y.F., Endress,G.A., Duan,R.D., Kyaw,H., Ebner,R., Lafleur,D.W., Olsen,H.S., Shi,Y. and Moore,P.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95 human secretory proteins Patent: JP 2002506627-A 25 05-MAR-2002; HUMAN GENOME SCIENCES INC
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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1 (bases 1 to 2120)

Ota, T., Nishikawa, T., Isogai, T., Hayashi, K., Ishii, S., Kawai, Y., Wakamatsu, A., Sugiyama, T., Nagai, K., Kojima, S., Otsuki, T. and
                                                                                                                                                                                                                 PC C12821/02.CLACH, NO. / CONTROL OF THE Primer for synthesizing full-length Location/Qualifiers

The Constitution (16) . (1089).
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JP 2002017375-A/3289.
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PI YURI KAWAI,AI WAKAMATSU,TOMOYASU SUGIYAMA,KEIICHI NAGAI,
SHINICHI KOJIMA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DA Ad OS
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TOSHIO OTA,TETSUO NISHIKAWA,TAKAO ISOGAI,KOJI HAYASHI,SHIZUKO
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JP 2002017375-A/3289
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                                  /organism="Homo sapiens"
/mol_type="genomic DNA"
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Homo sapiens cDNA FLJ90628 fis, clone PLACE1003407, highly similar
to Homo sapiens putative transmembrane protein (CLN5) mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center; CDNA 5'- & 3'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (25-MAR-2002) Takao Isogai, Helix Research Institute, Submitted (25-MAR-2002) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) NEDO human cDNA sequencing project supported by Ministry of NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan, cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction: Research Association for Biotechnology; cDNA library construction: Institute of Medical Science, University of Tokyo, Laboratory of
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/clone_Tib="PLACE1"
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Savukoski, M., Klockars, T., Holmberg, V., Santavuori, P., Lander, E.S.
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SYDCSKFVLRTFNKLAEFGAEEKNI ETNYTRI FLYSGEPTYLGNETSVFGPTGNKTLG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (29-MAY-1997) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, Ma 02141, USA On May 29, 1997 this sequence version replaced gi:1932720. The Staden databases, finishing information, and all chromatographic files used in the assembly of this clone are
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4361. .4640
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                                                       Conservative:
Mismatches:
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Matches:
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VERSION
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AL136440
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 162085 bases at least Q40
Consensus quality: 164521 bases at least Q30
Consensus quality: 166040 bases at least Q20
Insert size: 168062; sum-of-contigs
Insert size: 168062; sum-of-contigs
Ouality coverage: 4.08x in Q20 bases; sum-of-contigs Quality
Coverage: 4.16x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 requests: clonerequest@sanger.ac.uk
On Sep 8, 2000 this sequence version replaced gi:6982057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens chromosome 13 clone RP11-185I24, 14 unordered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
------ Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (10-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Burton, J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NOTE: This is a 'working draft' sequence. It currently consists of 14 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                 as soon as it is available and the accession number will be preserved.
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HTGS_PHASE1; HTGS_CANCELLED
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gap of 100 bp
contig of 12944 bp in length
                 gap of contig gap of contig
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contig of 2970 bp in length
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g of 2627 bp in length
of 100 bp
g of 3185 bp in length
of 100 bp in length g of 20568 bp in length of 100 bp in length bp if 100 bp in length of 100 bp
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of 25693 bp in length
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of 34450 bp in
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of 7444 bp in length
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7 147236: gap of 100 bp
7 164925: contig of 17689 bp in length
6 165025: gap of 100 bp
6 169362: contig of 4337 bp in length.
Location/Qualifiers
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fragment_chain:2
clone_end:SP6
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/clone_lib="RPCI-11.1"
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/mol type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="13"
                                                                                                                                                                                                                                                                                                                                                                                            /note="assembly_fragment:01198
fragment_chain:2"
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fragment_chain:1"
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fragment_chain:1"
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fragment_chain:1"
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Fragment_chain:2"
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fragment_chain:2"
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fragment_chain:2"
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ragment_chain:1"
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ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Assembly program: XGRP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 220597 bases at least Q40
Consensus quality: 234299 bases at least Q30
Consensus quality: 241103 bases at least Q20
Insert size: 245987; sum-of-contigs
Insert size: 190986; agarose-fp
Quality coverage: 2.52x in Q20 bases; sum-of-contigs Quality
coverage: 3.92x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (12-JUN-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Aug 22, 2000 this sequence version replaced gi:8894433.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@manger.ac.uk
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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HTG; HTGS_PHASE1; HTGS
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AL359875
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center project name: bA453N22
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63088: 63188: 65281: 65381: 67940: 68040: 75029: 75129:

63089 63189 65282 65382 679381 75030 75130 85568 89151 89251 89251 89251 89251 89251 100593 1104060 1104060 1104060 1115656 1115656 1115656 1118694 1123631 1123631

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8: contig of 6545 bp in length
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7. Gap of 100 bp
4. contig of 2497 bp in length
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6. gap of 100 bp
6. contig of 4874 bp in length
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/note="assembly_fragment:00469
fragment_chain:1"
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32331. .3
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/organism="Homo sapiens"
/mol_type="genomic DNA"
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52270. .
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/note="assembly_fragment:01288
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fragment_chain:1"
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63189. .65281
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fragment_chain:4"
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/db_xref="taxon:9606"
/chromosome="13"
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fragment_chain:2"
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fragment_chain:2"
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Thote="assembly fragment:00352
fragment_chain:1"
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/clone_lib="RPCI-11.2"
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56544. .63088
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fragment_chain:5"
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fragment_chain:4"
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ragment_chain:3"
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fragment_chain:3"
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fragment_chain:2"
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fragment_chain:5"
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234942: contig of 2322 bp in length
235042: gap of 100 bp
240958: contig of 5916 bp in length
241058: gap of 100 bp
251187: contig of 10129 bp in length.
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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> 15692; 15702;

16015

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206338 210377 210477 225246 225346 230028 230128

230027: 230127: 232610:

241265

204161 206238

210376: 210476: 194564 197683 197783 201789 201889

204060:

201888:

185016 187239 187339 189603

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18491

189703 194464

189702 194463 194563 166601 166701 171897 171997 148767 148867

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129685 129785 132133 132233 143793

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1 (bases 1 to 1038)
Sheppard, P.O. and Gilberton, D.G.
Secreted protein which human chromosome
Patent: JP 2001511345-A 12 14-AUG-2001;
                                                                                                                                                                                                   61 YTNTGGYTNGCNGTNGTNCCNGGNTGG
                                                                                                                                                                                                                             21 LeuTrpLeuAlaValValProGlyTrp
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BD073413.1 GI:22619016
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STS.
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 Yuen, K.Y.,
                            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Penici
                                                       Penicillium marneffei
Penicillium marneffei
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24-JUL-1997 US 60/053613
PAUL O SHEPPARD, DIBRA G GILBERTON
C12N15/09, A61K38/00, A61K48/00, C07K14/47, C07K16/18, C12N1/15,
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
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Danchin, A. and Pascal
Direct Submission
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During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submis sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., bared quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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                                                                                                                                                                                                                                                                                     Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
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/db_xref="taxon:37727"
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REFERENCE 2 (bases 1 to 256073) REFERENCE 2 (bases 1 to 256073) RUTHORS Daniels,R.J., Peden,J.F., Lloyd,C., Horsley,S.W., Clark,K., Tufarelli,C., Kearney,L., Buckle,V.J., Doggett,N.A., Flint,J. and Higgs,D.R. TITLE Direct Submission Submitted (07-DEC-2000) MRC Molecular Haematology Unit, Weatherall Institute of Molecular Medicine, John Radcliffe Hospital, Oxford, Coon OX3 9DS, UK FEATURES source /organism="Homo sapiens" /mol_type="genomic DNA"	NISM Homo Sapiens Bukaryota; Me Bukaryota; Me Mammalia; Eut 1 (bases 1 t ORS Daniels; R.J., Tufarelli, C., Higgs, D.R. Sequence, str Mb of the sho NAL Hum. Mol. Gen INE 21096910	BS-10-010-050A-2_COPY_1_30 (1-30) x HS444G9 (1-28835) W	(unpublished), and is from the Los Alamos, flow sorted human Chromosome 16 libraries constructed by Norman Doggett (unpublished). VECTOR: sCos-1. EATURES Location/Qualifiers Location/Qualifiers	assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; TT:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep LA16c-444G9 is part of a clone contig from the tip of the short arm of chromosoms part of a clone contig from the tip of the short arm of chromosoms of the short arm of the short arm of the short arm of the short arm of the short
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complement(10481. .10623)
note="MERE8; RepeatMasker predicted
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4193. .4497
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                                                /product="small optic lobes
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join(19075. .20523,21229. .21437,21524. .21707,21851. .22074,

22538. .23663,23748. .23900,24287. .24448.24537. .24766,

24841. .25007,25099. .25277,25575. .25752)
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translation="MATVGEWSCVRCTFLNPAGQRQCSICEAPRHKPDLNHILRLSVE"
               /db_xref="MIM:603267"
/db_xref="SPTREMBL:075808"
                                                                                                           codon_start=
                                                                                                                            'note="PubMed:9722942"
                                                                                                                                            gene="SOLH"
                                                                                                                                                                                                                                                                                                                                                                                                   3. .15414
e="AluJb; RepeatMasker predicted
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                                                                                                                                                                                                                                                                                                                                                                        family="SINE/Alu"
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KEYWORDS
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AL137007
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VERSION
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Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alignment Scores: Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
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JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUTHORS
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requests: clonerequest@sanger.ac.uk

on Jun 26, 2000 this sequence version replaced gi:8573795.

During sequence assembly data is compared from overlapping clones.

Where differences are found these are annotated as variations where differences are found these are annotated as variations to gether with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human DNA sequence from clone RP1-303F19 on chromosome 6q12 Contains fragments of a gene similar to the Notch (Drosophila) homolog, STSs and GSSs, complete sequence.
AL137007
AL137007.9 GI:8745064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 GlyAlaGlyAlaAlaArg---GlyArgAlaSerTrpCysTrpAlaLeuAlaLeuLeuTrp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1. (bases 1 to 105779)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (01-AUG-2000) Sanger Centre, Hinxton, Cambridgeshire CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Williams,S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HTG; Notch
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LRRRESMHVEQRRQTDEGEAKALWENI VAFCRENNUSFVDDSTPPEREVGFPACDSV
QQRVRQWLRQDEINCSVFRDHALWENI VAFCRENNUSFVDDSTPPEREVGFPACDSV
QQRVRQWLRPQEINCSVFRDHALWENI VAFCRENNUSFVDDSTPPEREVGFPACDSV
QQRVRQWLRPQEINCSVFRDHALWENI VAFCRENNUSFVDDSTPPERSVGFPACDSV
QQRVRQWLROPTRSLCAGCAGYQVRLCKDGTWTTULVDDMLFCDEAGCLLFSQAQRKQLAVAL
IEKALAKLHGSYFALQAGRAI EGLATITGAPCESLALQLSGTWREBPVDTDLTWAKM
IEKALAKLHGSYFALQAGRAI EGLATITGAPCESLALQLSGTWPEREPVDTDLTWAKM
IEKALAKLHGSYFALQAGRAI EGLATITGAPCESLALQLSGTWPEREPVDTDLTWAKM
IEKALAKLHGSYFALQAGRAI EGLATITGAPCESLALQLSGTWPETDYDQTRLERLRNPWG
ISKEAGFFLWGASCGGGRMKVDDSA VESLGLERPAYSILDVRDVQGTRLERLRNPWG
ISKEAGFFLWGASCGGGRMKVDDSA VESLGLERPAYSIDDVRYEDVDLCKVHSDWQE
RESWNGSWSDEWPHWFGHLKGELMPHGSSEGVFWMESVDDVDSHLLDLCILVFRAT
FGSGGHLSLGALLAHSKRAVKFVSCDVMLERGEFSAVVCCAFNHWGPPLFGTPAPQAS
SPSACVPRASPEPGETVLAVSSRLWNVEFVBAQFTLADAITLITESRGERHEGREG
MTCYYLTHGWAGLIVVVENRHPKAYLHVQCDCTDSFNVVSTRGSLRTQDSVPPLHRQV
LVILGQLEGNAGFSITHRLAHRKAAQAFLSDWTASKGTHSPPLTPEVAGLHGPRPL"

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/note="(GGA)n; 1
23/10/2000"
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SCSVCGGPRALSLPRIPPEALVVPEVVAPAGFHVVPAAPPGLJPGEGAEAUPPATSQ
GPAAEPEPPRVPPFSPFSSTLQMNPVFRSRREVPPQLQPPVPEAAQESSPSAGGRGAPQ
GSGWAGASRLAELLSGKRLSVLEEEATEGGTSRVEAGGSSTSGSDIIDLAGDTVRYTPA
SPSSPDFTTWSCAKCTLRNPTVAPRGSACGGSKLHGFQEHGEPPTHCPDCGANKPSPC
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/note="C-rich;
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Score:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RPI-303F19 is from the library RPGI-1 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see http://bacpac.med.buffalo.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Group.
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Group. Further information can be found at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  //www.sanger.ac.uk/HGP/Chr6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8916. .9626
/note="THE1A-internal repeat: matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3043. .3372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /map="q12"
/clone="RP1-303F19"
                                                                                                                                                                                                     /note="MLT2CA repeat: matches 5.complement(12882. .13318)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 consensus'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="L1PB3 repeat:
                                                                                                                                                             complement (12883.
                                                                                                                                                                                                                                                                                 note="AluJb repeat: matches 7. .301 of .1321..11388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="THE1B repeat: matches 1. .88 of consensus"
2222. .8930
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                                                                                  note="match:
2928. .13479
                                                                                                                                                                                    note="match: GSS: Em:AQ817672"
                                                                                                                                                                                                                                                                                                                                                                                                               0218. .10903
                                                                                                                                                                                                                                                                                                                                                                                                                              note="THE1A repeat: matches 1.
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                                                                                                                          2884. .13584
                                                                                                                                                                                                                                           2656. .13022
                                                                                                                                                                                                                                                                note="34 copies 2 mer tc 67% conserved"
                                                                                                                                                                                                                                                                                                                                              note="match: GSS: Em:AQ113885"
                                                                                                                                                                                                                                                                                                                                                                       0422. .10793
                                                                                                                                                                                                                                                                                                                                                                                      note="match: GSS: Em:AQ321138"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sensus"
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                                                                                                       GSS:
                                                                 GSS: Em:AQ003316"
                                                                                                                                                 GSS:
                         repeat: matches 459.
                                                                                                                                                                  .13322
                                                                                                         Em: B83082"
                                                                                                                                            Em:AQ450753"
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complement(18807. .19243)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17051. .17264
/note="MLT1-INTERNAL repeat: matches 990.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="L1 repeat: matches 3787.
/note="L1 repeat: matches 3787.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="L1MC2 repeat: matches 5489. .6312 of consensus" 22102. .22393 /note="AluJb repeat: matches 1. .293 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17349. .17779
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                                                                                                                                                                                                                                                                                                     30540. .30562 /note="Single clone region. Assembly confirmed by restriction digest"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19454. .20541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="MLT1E repeat: matches 310.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="THE1B repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="33 copies 2 mer ta 74% conserved"
                                                                                                                                                                                                                                                                                                                                                                                            /note="L1MEc repeat: matches 944. .1803 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                /note="11MEc repeat: matches 1672. .2271 of consensus"
28570. .29375
                                                                                                                                                                                                                                                                                                                                                                                                                                                     27441. .28042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="MER52A repeat: matches 191. .1755 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="L1 repeat: matches 4377.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1964. .21210
note="L1MEc repeat: matches 1424.
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note="MLT2B repeat: matches 1. .400 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="L1PA13 repeat: matches 5736. .6156 of consensus"
                                                                                                36069. .36886
/note="L1M4c repeat: matches 828. .1627 of consensus"
                                                                                                                                                      /note="L2 repeat: matches 1837. .2666 of consensus"
35947. .36061
                                                                                                                                                                                                                           33714. .34154
                                                                                                                                                                                                                                                                                                                                                              /note="AluSc repeat: matches 1.
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note="L1MA7 repeat: matches 5918, .6288 of consensus"
                                                                                                                                                                                                     note="match: GSS: Em:AQ114098"
                                                                                                                                                                                                                                         'note="L2 repeat: matches 1837.
                                                                                                                                                                                                                                                                          'note="AluSq repeat: matches 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="L1MEc repeat: matches 2278.
                              note="THEIB repeat: matches 1.
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                                                                   note="L2 repeat: matches 2631.
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.24449
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reent Similarity: 62.50%
set Local Similarity: 58.33%
ery Match: 44.97%
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jarch completed: April 25, 2004, 03:25:56
jb time : 652.083 secs
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                                                                                                                                 8 AlaArgGlyArgAlaSerTrpCysTrpAlaLeuAlaLeuLeuTrpLeuAlaValVal--- 26
                                                                                                                                                                                                                                                                                                                                                                                                         /note="L2 repeat: matches 2524. .2745 of consensus"
42616. .43264
/note="L2 repeat: matches 1594. .2287 of consensus"
43381. .43745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42264 .42473
                                                                                                                                                                                                                                                                                                            46593. .46654
/note="31 copies 2 mer at 67% conserved"
47286. .47467
/note="L2 repeat: matches 2555. .2737 of consensus"
                                                                                                                                                                                                                                                                                                                                                                               /note="match: GSS: Em:AQ224165"
46534. .46589
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Matches:
Conservative:
Mismatches:
Indels:
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Ommand line parameters:

Ommodel frame+ p2n.model -DEV=xlh

Q=/cgn2 1/USPTO_spool/USI0010050/runat 22042004 113204 27556/app_query.fasta_1.1372

Q=/cgn2 1/USPTO_spool/USI0010050/runat 22042004 113204 27556/app_query.fasta_1.1372

DB=EST -QFMT=fastap -SUPFIX=rst -MINMATCH=0.1 -TOOPCIL=0 -LOOPEXT=0

UNITS:Dits -START=1 -END=-1 -MATRIX=Diosum62 -TRANNS=human40.cdi -LIST=45

DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL

OUTFMT=pto -NCRM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000

USER=US10010050 @CGN 1 1 6283 @runat 22042004 113204 27556 -NCFU=6 -ICPU=3

NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOKS=100 -LONGLOG

NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOKS=100 -LONGLOG

DEV_TIMEDUT=120 -MARN TIMEDUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6

FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ALIGNMENTS

REFERENCE		ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION		DEFINITION	LOCUS	AL546472	RESULT 1
Mammatla; Eucheria; Filmaces; Cacarrilli, Tomarioce, Tomaces 1 to 1201)	Eukaryota; Metazoa; Chordata; Craniata; Vercebraca; Eucerecent,	Homo sapiens	Homo sapiens (human)	EST.	AL546472.2 GI:31268306	AL546472	clone CSODIO30YJ01 5-PRIME, mRNA sequence.	AL546472 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens come	AL546472 1201 bp mRNA linear Est Street		

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On Feb 15, 2001 this sequence version replaced
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Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7238.f For
more information about this cluster, see
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BP 191 91006 EVRY cedex - France
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Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
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Location/Qualifiers
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/clone_Tib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="Ist strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR v
sites of the pCMVSPORT 6 vector. Library was normalized.
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/db_xref="taxon:9606"
/clone="CS0DI030YJ01"
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                                                                                                                                                                                                                                             Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Komo,H., Okazaki,Y., Muzamatsu,M. and Hayashizaki,Y., Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new (denome Res. 10 (10), 1617-1630 (2000)
              Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y., RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
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High-efficiency full-length cDNA
Meth. Enzymol. 303, 19-44 (1999)
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                                                                                                                                                                                                                                                                                      Scores
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (16-ULI-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokoha Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome-gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Group Phase I & II Team.
Analysis of the mouse transcriptome of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 2356)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The FANTOM Consortium and the RIKEN
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Please visit our web site for further details.
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URL:http://fantom.gsc.riken.go.jp/
TyrCysGlnAlaLysTyrThrPheCysProThrGlySerProIleProValMetGluGly
                                                                                    SerArgArgHisTrpProValProTyrLysArgPheAspPheArgProLysProAspPro
                                                           Consortium.
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/clone="A730075N08"
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/db_xref="FANTOM_DB:A730075N08"
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 2247)
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
                                                                                                                                                                                                                                                                                              cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome
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                                                                                                                                                                     URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/
                                                                                                                                                                                                                 prepare mouse tissues.
Please visit our web site for further details
                                                                                                                                                                                                                                                                       Division of Experimental Animal Research
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/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="RANTOM_DB:6430516P20"
/db_xref="MGI:2395762"
                                                                                                                                                   Location/Qualifiers
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PheLysAsnIleGluThrAsnTyrThrArgIlePheLeuTyrSerGlyGluProThrTyr 226
                                                                                                                                             TATGAGACATGGACGGTCCGAGCCGGCCCAGGACAAGGGGCCCAGACGTGGTTCGAGTCC
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                                                                                    TyrAspCysSerLysPheValLeuArgThrPheAsnLysLeuAlaGluPheGlyAlaGlu
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                                               /proteIn_id="BAC27797.1"
/db_xref="G1:26328113"
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/tzms1ation="LGLATTILGASPTSGQRWPVPYKHFSFREKTDPYCQAKYTFCPTG
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FQLGWCTFPHLREDASAFFWCMQGAACFFEG1DDKHWKENGTLSVVAATISGNTFNKXVA
EWYKQDNETGIYYETWTVRAGPGQGAQTWFESYDCSWFVLKTYKKLAEFGTERKXIET
EWYKQDNETGIYYETWTVRAGPGQGAQTWFESYDCSWFVLKTYKKLAEFGTERKXIET
TYTKIFLYSGEBIYLGMSTSIGGBKGNKTLALAIKKFYGFFRYLSTKDFLMNFLKIF
DTVIIHRQFYLFYNFEXWFLFMKPPFVKITYEETPLPTRHTTFTDL"
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clone="6430516P20"
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'clone_lib="RIKEN full-length enriched mouse cDNA library"
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Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y., Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new g Genome Res. 10 (10), 1617-1630 (2000)
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AKO85741

AKO85741

Mus musculus 10 days lactation, adult female mammary gland cDNA, RIKEN full-length enriched library, clone:D730033P03

product:similar to CEROID-LIPOFUSCINOSIS NEURONAL PROTEIN 5 (CLN5
                                                                                                                                                                                                                                                                                                     Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                   The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
  Analysis
                             Group Phase
                                                        The FANTOM Consortium and the RIKEN Genome Exploration Research
                                                                                                                Nature 409,
                                                                                                                                              Functional
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I & II Team.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (16.APR-2002) Yoshihide Hayashizaki, The Institute of Submitted (16.APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Pax:81-45-503-9216)
                                                                                                                                                                                                                                       27
                 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 420, 563-573 6 (bases 1 to 2433)
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Please visit our web site for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.
        LeuLeuGlyHisLeuLysIleMetHisAspAlaIleGlyPheArgSerThrLeuThrGly
                                                                                                                   AspAspAspIleGluValPheArgLeuGlnAlaProValTrpGluPheLysTyrGlyAsp
                                                                                                                                                                                                                              TyrCysGlnAlaLysTyrThrPheCysProThrGlySerProIleProValMetGluGly
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                                                                    AATGACGTCATCGAGGTCTTACGACTACAAGCCCCGGATTTGGGAATTTAAATATGGAGAC
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/db_xref="MGI:2422937"
/db_xref="taxon:10090"
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(clone_lib="RIKEN full-length enriched mouse cDNA library"
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                                                                                                                                                                                                                                                BU621797 689 bp mRNA linear EST 23-SEP-U1-E-FL1-bgb-i-07-0-UI.sl NCI CGAP FL1 Homo sapiens cDNA clone UI-H-FL1-bgb-i-07-0-UI 3', mRNA sequence.
BU621797
BU621797.1 GI:23288012
                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 689)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
                                                                                                                                                                                                                                    EST.
                                                              Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                 Homo sapiens
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: James Martin
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
                                                                                               Tumor Gene Index
                                                                                                                   National Cancer Institute, Cancer Genome
                                                                                                                                                                                                                 Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TyrGluThrTrpAsnValLysAlaSerProGluLysGlyAlaGluThrTrpPheAspSer 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GlyIlaAspAspValHisTrpLysGluAsnGlyThrLeuValGlnValAlaThrIleSer 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LeuArgProGluMetAspAlaProPheTrpCysAsnGlnGlyAlaAlaCysPhePheGlu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LysAsnTyrThrMetGluTrpTyrGluLeuPheGlnLeuGlyAsnCysThrPheProHis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGAATAGATGATAAACACTGGAAGGAAAACGGGACACTGTCAGTCGTTGCAACCATATCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   TATTGGTTTCTACCAATGAAACCCCCCTTTGTCAAAATAACATACGAAGAAACCCCCGTTA
                                                                                                                    Anatomy
                                                                                                                   Project (CGAP),
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      AAGTTGGCTGAATTTGGAGCAGAGTTCAAGAACATAGAAACCAACTATACAAGAATATTT
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DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Clone distribution information can be from Dr. M. Bento Soares, bento-soares@ulowa.edu Seq primer: M13 FORWARD
                                                         / clone lib="NCI CGAP FLI"
//clone lib="NCI CGAP FLI"
//clone lib="NCI CGAP FLI"
//pharmacia) with a modified polylinker; Site 1: EcoR I;
(Pharmacia) with a modified polylinker; Site 1: EcoR I;
(Site 2: Not I; NCI CGAP FLI is a normalized CDNA library
derived from a pool of mRAA obtained from 4 cell lines
from grade III chondrosarcoma tissues. The library was
constructed according to Bonaldo, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA
synthesis was primed with an oligo-dT primer containing a
Not I site. Double stranded cDNA was ligated to an EcoR I
adaptor, digested with Not I, and cloned directionally
into pT/TI3-Pac vector. The oligonucleotide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(dT)18 tail. The sequence tag for this library is
GAGGTCGGTG. The cell lines were provided by Dr. James
Martin from the University of Iowa.

Martin from the University of Iowa.
                              TAG_TISSUE=Human Chondrosarcoma Grade 3 cell line mix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="UI-H-FL1-bgb-i-07-0-UI"
/fissue_type="Cell lines"
/dev_stage="Adult"
/lab_host="DH108_(Life_Technologies)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ocation/Qualifiers
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/db_xref="taxon:9606"
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LIB=UI-H-FL1
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В	VQ.	유 왕	Qу	d Q	Qy Db	Ωy Db	US-10-0	Alignment Pred. No. Score: Percent S Best Loca Query Mat DB:
388 GGGCAGAGACATGGTTTGATTCCTACGACTGTTCCAAATTTGTGTTAAGGACCTTTAAC	179 GlyAlaGluThrTrpPheAspSerTyrAspCysSerLysPheValLeuArgThrPheAsn	159 GlnAspAsnGluThrGlyIleTyrTyrGluThrTrpAsnValLysAlaSetProGluLys 	139 LeuvalGlnvalAlaThrIleSerGlyAsnMetPheAsnGlnMetAlaLysTrpValLys 	119 GlnglyAlaAlaCysPhePheGluGlyIleAspAspValHisTrpLySGluAsnGlyThr 	99 LeuGlyAsnCysThrPheProHisLeuArgProGluMetAspAlaProPheTrpCysAsn 	79 GlyPheArgSerThrLeuThrGlyLysAsnTyrThrMetGluTrpTyrGluLeuPheGln 	US-10-010-050A-2_COPY_31_346 (1-316) x BU621797	Alignment Scores: Pred. No.: 2.71e-127 Matches: 1237.00 Matches: 100.00\$ Percent Similarity: 100.00\$ Best Local Similarity: 98.67\$ Mismatches: 70.36\$ Query Match: 13 Gaps:
GTTCCAAAT	ysSerLysP 	hrTrpAsnV CATGGAATG	etPheAsnG TGTTCAACC	spaspvalh argargrrc	roGluMetA CTGAAATGG	YrThrMetG ACACAATGG	97 (1-689)	: ative: hes:
GGGCAGAGACATGGTTTGATTCCTACGACTGTTCCAAATTTGTGTTTAAGGACCTTTAAC	heValLeuArgThrPheAsn	allysalaSerProGluLys TAAAAGCCAGCCCAGAAAAG	InmetAlaLysTrpValLys	PheGluGlyIleAspAspValHisTrpLysGluAsnGlyThr 	spAlaProPheTrpCysAsn 1 	luTrpTyrGluLeuPheGln aaTGGTATGAACTTTTCCAA)	689 222 3 0 0

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CA488543
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National Institutes of Health, Mammalian
Unpublished (1999)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Plate: LLAM14279 row: j column:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDNA Library Preparation: Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Kristi A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (human)
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/mol type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6720309"
/cell_line="ZR-75-1, MCF7, S
                                                                                                                                                                            /lab host="MMDH109"
/clone lib="MAPCL"
/clone lib="MAPCL"
/clone lib="MAPCL"
/note="Vector: pCMV-SPORT6; Site_1: EcoRV; Site_2: Not I;
/note="Tvector: pCMV-SPORT6; Site_1: EcoRV; Site_2: Not I;
/note="Tvector: pCMV-SPORT6; Site_1: EcoRV; Site_2: Not I;
/note="Tvector: pcmv-sports of the property of the pcm-state of the pcm-stat
                                                                                                                                          cancer genes encoding membrane and secreted proteins.
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US-10-010-050A-2_COPY_31_346 (1-316) x CA488543 (1-924)
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BX331615 Homo sapiens NEUROBLASTOMA COT 10-NORMALIZED Homo
CDNA Clone CSODB009YC01 5-PRIME, mRNA sequence.
BX331615
Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7238.f For
more information about this cluster, see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Full-length cDNA libraries and normalization Unpublished (2001)
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Location/Qualifiers
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Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
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                                                                                                                                              AlaAlaCysPhePheGluGlyIleAspAspValHisTrpLysGluAsnGlyThrLeuVal
                                                                                                                                                                                        AANTGTANATTTCCCCCNTCTCCGNNCTGNAATGGRTGSSCCTTTCTGGKGTAATCAAGGG
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Clone CSODIO30YJ01 3-PRIME, mRNA sequence.
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Feng Liang Email : filang@lifetech.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DI030CE01NP1.
Location/Qualifiers
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On Feb 16, 2001 this sequence version replaced
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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more information about this cluster, see
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                                        TÍCAGAAGTACATTWACTGGCAARAM-TACAMAATGAATTGGTATGA-MTTTTCCAACTT
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/CIONE="CSODIO30YJ01"
/tissue type="PLACENTA COT 25-NORMALIZED"
/clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="Ist strand cDNA was primed with a NotI-oligo (dr)
/note="Ist strand cDNA was primed, double-strand cDNA was
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                 CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINI
CDNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information of
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM9579 row: b column: 08
High quality sequence stop: 662.
Location/Qualifiers
                                                                                                                      Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Butheria; Primates; Catarrhini; Hominidae;
I (bases 1 to 931)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collect
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601450425F1 NIH_MGC_65 Homo &
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/mol_type="mRNA"
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Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.8 kb. Library constructed by Life
Technologies. "
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red. No.: red. No.: core: ercent Similarit est Local Simila uery Match: B:	Scores: 3.12e-124 Length: 931 1211.00 Matches: 232 milarity: 93.57% Conservative: 1 . Similarity: 93.17% Mismatches: 14 . Similarity: 93.17% Indeals: 4 . Gaps: 1 1
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ъ _В	67 LeuLeuGlyHisLeuLysIleMetHisAspAlaIleGlyPheArgSerThrLeuThrGly 86
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JOURNAL
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Tissue Procurement: ATCC
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                                                                                                                                                                      GluPheLysTyrGlyAspLeuLeuGlyHisLeuLysIleMetHisAspAlaIleGlyPhe
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Li, W.B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization Unpublished (2001)
                                                                                                                                                                                                                          Genoscope - Centre National de Sequencage
Bap 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7238.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSOBAG053ZH03 CSO5016 l&cluster=7238.f.
Contact: Feng Liang Email: fliang@lifetech.com URL:
Contact: Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSOBAG053ZH03_CSO5016_1.
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/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR _{\rm c}
                                                                      /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DL004YP03"
/cell_type="B CELLS (RAMOS CELL LINE) COT 25-NORMAI
/cell_line="RAMOS CELL LINE"
/clone_lib="Homo sapiens B CELLS (RAMOS CELL LINE)
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CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIN
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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NIH-MGC http://mgc.nci.nih.gov/
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Tissue Procurement: DCTD/DTP
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Contact: Robert Strausberg, Ph.D.
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{\tt GlyAsnMetPheAsnGlnMetAlaLysTrpValLysGlnAspAsnGluThrGlyIleTyr}
                                                                                    GlyIleAspAspValHisTrpLysGluAsnGlyThrLeuValGlnValAlaThrIleSer
                                                                                                                                                                              LeuArgProGluMetAepAlaProPheTrpCysAsnGlnGlyAlaAlaCysPhePheGlu
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                                                                                                                                                                                                                                                                                                                                                                   LeuLeuGlyHisLeuLysIleMetHisAspAlaIleGlyPheArgSerThrLeuThrGly
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/lab host="PHIOB (phage-resistant)"
/clone_lib="NIH_MGC_40"
/clone_lib="NIH_MGC_40"
/note="Torgan: prostate; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming-
pirectionally cloned into EcoRI/XhoI sites using the
following 5 adaptor: GGCACGAG(G). Library constructed by
fing Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6382620"
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RESULT 13
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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602976736F1 NCI_CGAP_Mam2 Mus musculus cDNA clone IMAGE:5008544 5',
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BI080303.1 GI:14498633
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http://image.llnl.gov
plate: LiAMil1053 row: g column:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                     Email:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D
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                                                                                                                                                                                                                                           quality sequence stop:
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                      cgapbs-r@mail.nih.
/note="Organ: mammary; vector: pCMV-SPORT6; Site 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Öligo dT. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"
                                                                  /clone="IMAGE:5008544"
/tissue_type="tumor, biopsy
/dev_stage="5 months"
/lab_host="PHIOS"
/clone_lib="NCI_CGAP_Mam2"
                                                                                                                                                         /mol_type="mRNA"
/strain="FVB/N-3"
/db_xref="taxon:10090"
                                                                                                                                                                                                            organism="Mus musculus"
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                                                                                                                                                                                   AATTC-TTGACAACTTTTGATACAGTGATTTTACACCAGACAGGTCTACTGGTTTTATAA
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Mammalia; Eutheria; Primates; Catarrhini;
1 (Mases 1 to 787)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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Tissue Procurement: ATCC
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Contact: Robert Strausberg, Ph.D
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/note="Torgan: cervix; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.4 kb. Library prepared by Life
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Sequencing Center (NISC)
Clone distribution: NCI-CGAP clone distribut
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                                                                                                                                                                                                               /tissue_type="normal endometrium, phase, Gycle day 13" /lab_host="DH10B (T1-resistant)"
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Search comple	Db 5	0у 1	5 da	Q y 16	Db 4	Qy 1	Db 40	07 1	Db 34	0у 1	Db 2	<i>Y</i> Q	Db 2	Qy	pb 1	Qy	Db 1	Qy	Db	Qy	US-10-010-0	Alignment Scores: Pred. No.: Score: Percent Similarity: Best Local Similarity: Query Match: DB:
leted: April 25, 2004, 05:46:13	82 GAGACATGGTTTGATTCCTACGACTGTTCCAAATTTGTGTTAAGGACCTTTAACAAGTTG 541	81 GluThrTrpPheAspSerTyrAspCysSerLysPheValLeuArgThrPheAsnLysLeu 200	22 AATGAAACAGGAATTTATTATGAGACATGGAATGTAAAAGCCAGCC	J-1	62 CAAGTAGCAACTATATCAGGAAACATGTTCAACCAAATGGCAAAGTGGGTGAAACAGGAC 521	141 GlnValAlaThrIleSerGlyAsnMetPheAsnGlnMetAlaLysTrpValLysGlnAsp 160	02 GCTGCCTGCTTTTTGAGGGAATTGATGATGTTCACTGGAAGGAA	121 AlaAlaCysPhePheGluGlyIleAspAspValHisTrpLysGluAsnGlyThrLeuVal 140	42 AACTGTACATTTCCCCATCTCCGACCTGAAATGGATGCCCCTTTCTGGTGTAATCAAGGC 401	101 AsnCysThrPheProHisLeuArgProGluMetAspAlaProPheTrpCysAsnGlnGly 120	82 AGAAGTACATTAACTGGCAAGAACTACACAATGGAATGG	81 ArgSerThrLeuThrGlyLysAsnTyrThrMetGluTrpTyrGluLeupheGlnLeuGly 100	22 GAATTTAAATATGGAGACCTCCTGGGACACTTGAAAATTATGCATGATGCCATTGGATTC 281	61 GluPheLysTyrGlyAspLeuLeuGlyHisLeuLysIleMetHisAspAlaIleGlyPhe 80	62 ATCCCAGTTATGGAGGGTGATGATGACATTGAAGTTTTTCGATTACAAGCCCCAGTATGG 221	41 IleProValMetGluGlyAspAspAspIleGluValPheArgLeuGlnAlaProValTrp 60	102 CGTCCAAAACCTGATCCTTATTGTCAAGCTAAGTATACTTTCTGTCCAACTGGCTCACCT 161	21 ArgProLysProAspProTyrCysGlnAlaLysTyrThrPheCysProThrGlySerPro 40	42 CGGGTCTCGGGCATCCCCTCCCGGCGCCACTGGCCGGTGCCCTACAAGCGCTTTGACTTC 101	1 ArgValSerGlyIleProSerArgArgHisTrpProValProTyrLysArgFheAspPhe 20	050A-2_COPY_31_346 (1-316) x CB215456 (1-641)	Cores: 4.52e-116 Length: 641 1136.00 Matches: 200 iilarity: 100.00% Conservative: 0 Similarity: 100.00% Mismatches: 0 64.62% Indels: 0 14. Gaps: 0

Search completed: April 25, 2004, 05:46:13 Job time: 4028.01 secs

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Minimum DB
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-Q=/cgn2 1/USFTO_spool/US10010050/runat 22042004 113205 27584/app_query.fasta_1.1372
-Q=/cgn2 1/USFTO_spool/US10010050/runat 22042004 113205 27584/app_query.fasta_1.1372
-DB=-Published_Applications_NA -QFMT=fastap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANNS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXIEN=2000000000 -USER-US10010050_@CGN 1 776_@runat 22042004 113205_27584
-NCPU=6 -LOCPU=3 -NO_MMAp -LARGEQUERY -NEG SCORES=0 -WAIT -DSSPBLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXI=7
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and is derived by analysis of the total
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/ cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
/ cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
/ cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
/ cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
/ cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
/ cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
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Sequence 253, Appli Sequence 4, Appli Sequence 23914, A Sequence 1, Appli Sequence 22862, A Sequence 43789, A Sequence 16281, A Sequence 36547, A	1, App 94, 94, 91,	e 2753, e 37401 e 2159, e 159, e 159, e 127, e 127, e 127, e e 2256 e 2, Apre e 2, Apre e 12, Apre	quence 1, Appl equence 26, Ap equence 26, Ap equence 26, Ap parties 26, Ap parties 13, App equence 13, Ap quence 2559, equence 5835, A quence 5835, A quence 1859, quence 1863, A equence 1363, A equence 1363, A

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ALIGNMENTS

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RESULT 1
US-09-122-383-1
US-09-122-383-1
; Sequence 1, Application US/09122383A
; Patent No. US20020042093A1
; GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
APPLICANT: Gilbertson, Debra G.
ITILE OF INVENTION: CHROMOSOME 13
FILE REFERENCE: 97-38
CURRENT APPLICATION NUMBER: US/09/122,383A
CURRENT FILING DATE: 1998-07-24
CURRENT FILING DATE: 1998-07-24
EARLIER APPLICATION NUMBER: 60/053,613
EARLIER APPLICATION NUMBER: 60/053,613
EARLIER OF SEQ ID NOS: 19
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1
LENGTH: 1486
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: CDS
LOCATION: (47)...(1084)
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Result

Score

Query Match Length DB

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Description

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Best Local Similarity:
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Best Local Similarity:
Query Match:
DB:
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LENGTH: 1486
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APPLICANT: Gilbertson, Debra G.
TITLE OF INVENTION: SECRETED PROTEINS ENCODED
TITLE OF INVENTION: CHROMOSOME 13
FILE REFERENCE: 97-38C1
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NAME/KEY: CDS
LOCATION: (47)...(1084)
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ORGANISM: Homo
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                               CAAGTAGCAACTATATCAGGAAACATGTTCAACCAAATGGCAAAGTGGGTGAAACAGGAC
                                                 AACTGTACATTTCCCCATCTCCGACCTGAAATGGATGCCCCTTTCTGGTGTAATCAAGGC
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CURRENT APPLICATION NUMBER: US/10/653,595
CURRENT FILING DATE: 2003-09-03
PRIOR APPLICATION NUMBER: US 09/397945
PRIOR APPLICATION NUMBER: US 09/397945
PRIOR APPLICATION NUMBER: PCT/US99/05804
PRIOR APPLICATION NUMBER: E0/078,566
PRIOR APPLICATION NUMBER: 60/078,566
PRIOR APPLICATION NUMBER: 60/078,576
PRIOR FILING DATE: 1998-03-19
PRIOR PILING DATE: 1998-03-19
PRIOR PILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/078,573
PRIOR APPLICATION NUMBER: 60/078,574
PRIOR APPLICATION NUMBER: 60/078,579
PRIOR APPLICATION NUMBER: 60/080,314
PRIOR PRIOR PRIOR DATE: 1998-03-19
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                                                                                SEQ ID NO 26
LENGTH: 1751
TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                                              Remaining Prior Application data removed
NUMBER OF SEQ ID NOS: 470
SOFTWARE: PatentIn Ver. 2.0
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PRIOR APPLICATION NUMBER: 60/080,312
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/078,578
PRIOR APPLICATION NUMBER: 60/078,578
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FEATURE:
NAME/KEY: SITE
LOCATION: (1520)
OTHER INFORMATION: n equals a,t,g,
FEATURE:
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US-09-397-945-26
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PRIOR FILING DATE: 1999-03-18
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/078,566
PRIOR APPLICATION NUMBER: 60/078,576
PRIOR APPLICATION NUMBER: 60/078,573
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/078,573
PRIOR APPLICATION NUMBER: 60/078,574
PRIOR APPLICATION NUMBER: 60/078,574
PRIOR APPLICATION NUMBER: 60/078,579
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/080,314
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/080,314
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/078,578
PRIOR APPLICATION NUMBER: 60/078,578
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PRIOR APPLICATION NUMBER: 60/078,578
PRIOR PILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/078,581
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/078,577
PRIOR APPLICATION NUMBER: 60/078,563
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/078,563
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LENGTH: 1751
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CURRENT FILING DATE: 1999-09-17
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                                                                                   FEATURE:
NAME/KEY: SITE
LOCATION: (1520)
OTHER INFORMATION: r
                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 470 SOFTWARE: Patentin Ver. 2.0
                                 NAME/KEY: SITE
LOCATION: (1557)
OTHER INFORMATION:
                                                                                                                                                     TYPE: DNA
ORGANISM: Homo sapiens
                NAME/KEY:
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           ACTCTTGGTTTAGCCATAAAAAGATTTTATTACCCCTTCAAACCACATTTGCCAACTAAA
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APPLICANT: Sheppard, Paul O.
APPLICANT: Gilbertson, Debra G.
TITLE OF INVENTION: SECRETED PROTEINS ENCODED BY
TITLE OF INVENTION: CHROMOSOME 13
TILE REFERENCE: 97-38
FILE REFERENCE: 97-38
CURRENT APPLICATION NUMBER: US/09/122,383A
CURRENT FILING DATE: 1998-07-24
EARLIER APPLICATION NUMBER: 60/053,613
EARLIER FILING DATE: 1997-07-24
NUMBER OF SEQ ID NOS: 19
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US-09-122-383-13
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Patent No. US20020042093A1
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LOCATION: (1)...(1038)
OTHER INFORMATION: n is
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                                                       SerThrLeuThrGlyLysAsnTyrThrMetGluTrpTyrGluLeuPheGlnLeuGlyAsn
                                                                                                 TTYAARTAYGGNGAYYTNYTNGGNCAYYTNAARATHATGCAYGAYGCNATHGGNTTYMGN
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CURRENT APPLICATION NUMBER: US/10/010,050A
CURRENT FILING DATE: 2002-03-26
PRIOR APPLICATION NUMBER: US 09/122,383
PRIOR FILING DATE: 1998-07-24
PRIOR APPLICATION NUMBER: US 60/053,613
PRIOR FILING DATE: 1997-07-24
NUMBER OF SEQ ID NOS: 19
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13
LENGTH: 1038
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US-10-010-050A-13
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                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Sheppard, Paul O.
APPLICANT: Gilberteon, Debra G.
TITLE OF INVENTION: SECRETED PROTEINS ENCODED BY HUMAN
TITLE OF INVENTION: CHROMOSOME 13
FILE REFERENCE: 97-38C1
                                                                                        FEATURE: OTHER INFORMATION: Degenerate nucleotide sequence encoding zsig46 OTHER INFORMATION: polypeptide of SEQ ID NO:2
                                                                                                                                                ORGANISM: Artificial Sequence
                                                                                                                                                                     TYPE: DNA
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PRIOR FILING DATE: 2000-02-04
PRIOR PPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-10-04
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SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
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CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
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APPLICANT: Chen, Wensheng
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICHOARRAY
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICHOARRAY
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OR APPLICATION NUMBER: PCT/US01/0064

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OR FILING DATE: 2000-10-04
OR APPLICATION NUMBER: US 60/236,359
OR FILING DATE: 2000-09-27
OR APPLICATION NUMBER: PCT/US01/00666
OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: PCT/US01/00667
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APPLICATION NUMBER: US 60/234,687
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Hanzel, David K.
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                                                                                         N: EXPRESSED IN PLACENTA, SIGNAL = 4.5

N: EXPRESSED IN BRAIN, SIGNAL = 6.3

N: EXPRESSED IN BOUS MARROW, SIGNAL = 5.8

N: EXPRESSED IN ADULT LIVER, SIGNAL = 5.8

N: EXPRESSED IN LUNG, SIGNAL = 3.6

N: EXPRESSED IN HELA, SIGNAL = 3.9

N: EXPRESSED IN HEART, SIGNAL = 4.2

N: EXPRESSED IN FETAL LIVER, SIGNAL = 5.3

N: SWISSPROT HIT: 075503, EVALUE 2.00e-96

N: SWISSPROT HIT: H01255.1, EVALUE 0.00e+00
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: 2001-01-30
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2000-06-30
US 09/774,
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RESULT 8
US-10-040-739-825
; Sequence 825, Application No. US20020;
; Publication No. US20020;
; GENERAL INFORMATION;
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DB:
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Pred. No.:
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                                                                                                                                                                                                             Merberg, David
Treacy, Maurice
Spaulding, Vikki
TITLE OF INVENTION: SECRETED, I
NUMBER OF SEQUENCES: 1519
CORRESPONDENCE ADDRESS:
 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy Disk

COMPUTER: IBM PC COmpatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         174 AlaSerProGluLysGlyAlaGluThrTrpPheAspSerTyrAspCysSerLysPheVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       154 AlaLysTrpValLysGlnAspAsnGluThrGlyIleTyrTyrGluThrTrpAsnValLys 173
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                                                                                                                        ADDRESSEE: Genetics Institute,
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A
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LaVallie, Edward
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Indels:
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; MOLECULE TYPE: CDNA
; SEQUENCE DESCRIPTION: SEQ ID
US-10-040-739-825
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              GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Aeomica-X-1
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CURRENT APPLICATION NUMBER: US/09/864,761
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REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 09/036,520 FILING DATE: 03-JUN-1998 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                        ThrLeuGlyLeuAlaIleLysArgPheTyrTyrProPhe 253
                                                                                                                                                                                                                                                ACTOTTGGTTTAGCCATAAAAAGATTTTATTACCCCTTC 497
                                                                                                                                                                                                                                                                                                                                              SerGlyGluProThrTyrLeuGlyAsnGluThrSerValPheGlyProThrGlyAsnLys
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TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/10/040,739 FILING DATE: 07-Jan-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
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727.00
100.00%
100.00%
41.35%
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Matches:
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Indels:
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278

338

458 240 398 220 158

140

PROBES USEFUL

FOR

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FEATURE:

FEATURE:

OTHER INFORMATION: MAP TO ACO01226.1

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 4.5

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 6.3

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 5.0

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 5.0

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.6

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.9

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 4.2

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 4.2

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 5.3
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Query Match:
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PRIOR APPLICATION N
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PRIOR APPLICATION NUMBER: US 09/632,366
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TYPE: DNA
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FILING DATE: 2001-01-30
ADDITION NUMBER: PCT/US01/00664
ADDITION DATE: 2001-01-30
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APPLICATION NUMBER: PCT/US01/00668
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APPLICATION NUMBER: PCT/US01/00666
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APPLICATION NUMBER: PCT/US01/00662
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                      AlaThrIleSerGlyAsnMetPheAsnGlnMetAlaLysTrpValLysGlnAspAsnGlu
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RESULT 10
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SEQ ID NO 1859
LENGTH: 497
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Publication No. US20040005579A1
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FEATURE:
NAME/KEY: misc_feature
LOCATION: (2)...(2)
LOCATION: n eq
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TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PA133P1
CURRENT APPLICATION NUMBER: US/10/264,049
CURRENT FILING DATE: 2002-10-04
PRIOR APPLICATION NUMBER: PCT/US01/18569
PRIOR FILING DATE: 2001-06-07
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PRIOR FILING DATE: 2000-06-07
NUMBER OF SEQ ID NOS: 4360
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NAME/KEY: misc_feature
LOCATION: (295)..(295)
OTHER_INFORMATION: n equals
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LOCATION: (285)..(285)
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OTHER INFORMATION: n e
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                          NAME/KEY: misc feature LOCATION: (331)..(331)
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           LOCATION: (331)..(331)
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                                                                                          NAME/KEY: misc_feature
LOCATION: (323)..(324)
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         CURRENT APPLICATION NUMBER: US/09/867,701
CURRENT FILING DATE: 2001-05-29
NUMBER OF SEQ ID NOS: 10912
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2579
LENGTH: 351
                                                                                                                                                                                              Sequence 2579, Application US/09867701 Patent No. US20020132237A1 GENERAL INFORMATION:
                                                                                                 APPLICANT: Aglate, Paul A.
APPLICANT: Jones, Robert
APPLICANT: Harlocker, Susan L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.497
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OTHER INFORMATION: n equals
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PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: US/60/234,052
PRIOR FILING DATE: 2000-09-20
PRIOR APPLICATION NUMBER: US/60/234,923
PRIOR FILING DATE: 2000-09-25
PRIOR FILING DATE: 2000-09-25
PRIOR FILING DATE: 2000-09-25
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION
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CURRENT FILING DATE: 2001-09-18
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TITLE OF INVENTION: Process
TITLE OF INVENTION: Sets
                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: 689290-76
                                                   FILING DATE: 2000-09-27
APPLICATION NUMBER: US/60/235,840
FILING DATE: 2000-09-27
                                                                                                  APPLICATION NUMBER: US/60/235,711
FILING DATE: 2000-09-27
APPLICATION NUMBER: US/60/235,720
                                                                                                                                                                          APPLICATION NUMBER: US/60/235,637
FILING DATE: 2000-09-26
APPLICATION NUMBER: US/60/235,638
                 APPLICATION NUMBER: US/60/235,863 FILING DATE: 2000-09-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AspAsnGluThrGlyIleTyrTyrGluThrTrpAsnValLysAlaSerProGluLysGly 179
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NOS: 2276
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AND METHODS PREVENTION,

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; SOFTWARE: PatentIn versio
; SEQ ID NO 1363
; LENGTH: 473
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-954-456-1363
                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/908,975
CURRENT FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: US 60/287,724
PRIOR FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: US 60/221,607
PRIOR APPLICATION NUMBER: US 60/221,607
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 32337
SOPTWARE: PatentIn version 3.0
SEQ ID NO 10339
LENGTH: 60
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US-10-198-846-9753/c
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Best Local Similarity:
Query Match:
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Publication No. US20030165843A1
GENERAL INFORMATION:
APPLICANT: SHOSHAN, Avi
APPLICANT: WASSERMAN, Alon
APPLICANT: WASSERMAN, Alon
APPLICANT: MINIZ, Eli
APPLICANT: MINIZ, Liat
APPLICANT: FAIGLER, Simchon
TITLE OF INVENTION: OLICONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPT'S AND SPLICE
FILE REFERENCE: 36688-0005
FILE REFERENCE: 36688-0005
FILE REFERENCE: 36688-0005
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                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Homo sapiens
                                                                          102 CysThrPheProHisLeuArgProGluMetAspAlaProPheTrpCysAsnGlnGly 120
       9753,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    313
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     Application US/10198846
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; GENERAL INFORMATION:
APPLICANT: Lillie, James
; APPLICANT: Lillie, James
; APPLICANT: Xu, Yongyao
APPLICANT: Wang, Youzhen
; APPLICANT: Steinmann, Kathleen
; APPLICANT: Steinmann, Kathleen
; TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PRI
; TITLE OF INVENTION: THERAPY OF BREAST CANCER
; TITLE OF INVENTION THERAPY OF BREAST CANCER
; TILL REFERENCE: MRI-049
; CURRENT APPLICATION NUMBER: US/10/198,846
; CURRENT FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/306,220
; PRIOR FILING DATE: 2001-07-18
; NUMBER OF SEQ ID NOS: 14084
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Best Local Similarity:
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LOCATION: 2667
OTHER INFORMATION: n =
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TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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                                                                                                                                                                                  1344 ATCACTGTTCAAATATGTGGCAAGGTGAGGCTCTCTGTCCCCCTTTACCAGGAGCACGGA 1285
                                                                                                                                                                                                                                                                                                                                       1455 AGCCTTCTCCAGAGTGTTTGCGACTCACGGTCCAACATGTCCCAACAAA-----ACGCAA 1402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1554 CAACATGGACCAGCCCCACAGCTGAGGCCATCTCCTCACTGAGCCTGGGACCAGGTCCAC 1495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1674 CCCTGGCCCGGGCCTCCTTGTGCACACACCCAGGCCTTCCCCAGAACACGAGAGCACCGGG 1615
                                                                                                                                                                                                                                                           1401 GGGTGTTCTGCTCTTTACTAAATA---ÄÄCGTTCCCTTCCCAGAAACCAGCCCCAAACTC 1345
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                                                                                                                                                                                                                                                                                              92 GluTrpTyrGluLeuPheGlnLeuGlyAsnCysThrPheProHisLeuArgProGlu--- 110
                                                                                                                                                                                                                                                                                                                                                                       72 LysIleMetHisAspAlaIleGlyPheArgSerThrLeuThrGlyLysAsnTyrThrMet 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22
leSerGlyAsnMetPheAsnGlnMetAlaLys---
                                     TrpCysAsnGlnGlyAlaAlaCysPhePheGluGly-----
                                                                                                                                                                                                                                                                                                                                                                                                              GTAATGTGTCTTCAGTCCCCG---TGGGAATGG-----
                                                                                                             TGGTGTCTGCAAGGCAGTGCCTCTGAGTGTCAGGGAGATGGCCCCTCAGGCTCCCAAACC 1225
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ValPheArgLeuGlnAlaProValTrpGluPheLysTyrGlyAspLeuLeuGlyHisLeu 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----SerProlleProValMetGluGlyAsp-----
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                                                                      -----IleAspAspValHis--TrpLysGluAsnGlyThrLeuValGlnValAlaThrI 145
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30.72%
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Indels:
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Conservative:
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2667 70 32 109 121

----TGGCATCTC

1456

AspAspIleGlu

51

38

34

---TrpValLysG 159

127

115

 29 155
 2y 138 ThrLeuValGlnValAlaThrIleSerGlyAsnMetPheAsnGlnMetAla 154
JS-10-010-050A-2_COPY_31_346 (1-316) x US-10-369-493-36401 (1-986)
 #Alignment Scores: 0.0287 Length: 986 ### 986
 ; SEQ ID NO 36401 ; SEQ ID NO 36401 ; LENUTH: 986 ; TYPE: DNA ; ORGANISM: Aspergillus nidulans US-10-369-493-36401
 ; CURRENT APPLICATION NUMBER: US/10/369,493 ; CURRENT FILING DATE: 2003-02-28 ; PRIOR APPLICATION NUMBER: US 60/360,039 ; PRIOR FILING DATE: 2002-02-21
 ; APPLICANT: Goldman, Barry S. ; APPLICANT: Chen, Xianfeng ; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF ; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES ; FILE REFERENCE: 38-10(52052)B
 RESULT 15 US-10-369-493-36401 ; Sequence 36401, Application US/10369493 ; Publication No. US20030233675A1
 Db 873 TCTGCAGCAATTTTATTCTTTTCCAGTCTTTT 842
 Qy 275 alHisLysGlnPheTyrLeuPheTyrAsnPhe 285
 CICC
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Db 1001 ::001
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1110 CACAGCACGAGCCAGGTTCCAGGCAGAGGCTGTGGCAAACATTGTCATCGCCCATG
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                   259 ThrLysGluPheLeuLeuSerLeuLeuGlnIlePheAspAlaValIleVal 275
                                                        462 CACCCATTGGGCGCTTAGGCTTCGCCAGG-----TGGGCGTTTGAGGTTGAGATGCAG 515
                                                                                  239 AsnLysThrLeuGlyLeuAlaIleLysArgPheTyrTyrProPheLysProHisLeuPro 258
                                                                                                               219 LeuTyrSerGlyGluProThrTyrLeuGlyAsnGluThrSerValPheGlyProThrGly 238
                                                                                                                                                                                                                                   348 AGACTCGAT-----ATGTCCGGC 365
                                                                                                                                                                                                                                                            183 TrpPheAspSerTyrAspCysSerLysPheValLeuArgThrPheAsnLysLeuAlaGlu 202
                                                                                                                                                                                                                                                                                         163 ThrGlyIleTyrTyrGluThrTrpAsnValLysAlaSerProGluLysGlyAlaGluThr 182
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Search completed: April 25, 2004, 06:14:09 Job time: 636.806 secs

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Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh
-Q=/cgn2_1/USF70_spool/US10010050/runat 22042004 113205 27569/app_query.fast:a_1.1372
-DB=Issued Pateents NA -QFMT=fastcap -SUFFTX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=Dits -START=1 -END=-1 -MATRIX-blosum62 -TRANS-human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALICN=15
-MODE=LOCAL -OUTFMT=pto -NORM=sext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10010050 @CGN 1_1_140 @runat 22042004 113205 27569 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DSF TIMEDUT=120 -WARN_TIMEDUT=30 -THREADS=1 -XGAPDF=10 -XGAPEXT=0.5 -FGAPDP=6
-FGAPEXT=7 -YGAPDP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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No.
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Listing first 45 summaries
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length: 2000000000
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Ygapop 10.0,
Fgapop 6.0,
Delop 6.0,
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/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
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US-08-290-448A-73

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US-08-175-069A-73

US-08-461-039B-73

US-08-464-000-73

US-08-290-448A-58

US-08-290-448A-58

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US-08-461-939B-58

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Sequence 2, Appli
Sequence 244, App
Sequence 73, Appl
Sequence 58, Appl
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GENERAL INFORMATION:
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ALIGNMENTS

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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/108,006C
FILING DATE: 30-7un-1992
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Kimeragen,
STREET: 300 Pheasant )
                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Steer,
                                     APPLICATION NUMBER: 60/054,837
FILING DATE: 05-AUG-1997
APPLICATION NUMBER: 60/064,996
FILING DATE: 10-NOV-1997
APPLICATION NUMBER: 60/074,497
                                                                                                            APPLICATION NUMBER: 60/054,288 FILING DATE: 30-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Newtown
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Bandyopadhyay, Paramita
Roy-Chowdhury, Jayanta
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Query Match:
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                    121 aAlaCysPhePheGluGlyIleAspAspValHisTrpLysGluAsnGly---ThrLeuVa
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REFERENCE/DOCKET NUMBER: 7991-015-999
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                 101
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                                                                                                                                                                                                    AGAAGTGTCTTCAAAGCTGAGAAGAAATCTGCAGGACCATGCTGAGTGGGTTATCAA--
                                                                                                                                                                                                                                                                                                                                                                          nCysThrPheProHisLeuArgProGluMetAspAlaProPheTrpCysAsnGlnGlyAl 121
                              uAlaGluPheGlyAlaGluPheLysAsnIleGluThrAsn---TyrThrArgIlePheLe
                                                                                                aGluThrTrpPheAspSerTyrAspCysSerLysPheValLeuArgThrPheAsnLysLe
                                                                   CAGTGGGACCACTGGGACCTACCAA----
                                                                                                                                                                  pAsnGluThrGlyIleTyrTyrGluThrTrpAsnValLysAlaSerProGluLysGlyAl 180
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TYPE: nucleic acid
STRANDEDNESS: single
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GAGTGGAAGGACAAGGCCCAGAATCTGTACCAGGAACTGTTGAC ::2548
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Matches:
Conservative:
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Indels:
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APPLICANT: Furness, Michael
APPLICANT: Buchbinder, Jenny
TITLE OF INVENTION: GENES EXPRESSED IN C3A I
FILE REFERENCE: PA-0041 US
CURRENT PILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: 05/240,409
PRIOR FILING DATE: 2000-10-12
PRIOR FILING DATE: 2000-10-12
VINNBER OF SEQ ID NOS: 1143
SOFTWARE: PERL Program
SEQ ID NO 244
LENGTH: 7718
TYPE: DNA
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                       Query Match:
                                                                                                                                                                                                                                                                                                                                                                  Pred.
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Patent No. 6673549
GENERAL INFORMATION:
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LOCATION: 6339-6362, 6967-7026
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                  No.:
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3563 ATGGATGAGGACTTTTGCAGTCGCCTGAGGGAAGGCATGAGGATGAGAGCTCCTGAGTAC 3622
                                                                         3503 TACGGAGTATTGCTGTGGGAAATCTTCTCCTTAGGTGGGTCTCCATACCCAGGAGTACAA
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                                     46 GlyAspAspAspIle-
                                                                                                              29 GlnAlaLysTyr----
                                                                                                                                                                                    11 TrpProValProTyrLysArgPheAsp-----PheArgProLysProAspProTyrCys
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91.50
31.40%
20.64%
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                                                                                                              ----ThrPheCysProThrGlySerProIleProValMetGlu 45
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Matches:
Conservative:
Mismatches:
Indels:
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UESULT 3
IS-08-290-448A-73
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                                                                                                            GENERAL INFORMATION:
APPLICANT: Rogers, Bruce
APPLICANT: Klapper, David G.
APPLICANT: Rafnar, Thorum
                                   APPLICANT: Kuo, Mei-chang
TITLE OF INVENTION: Allergenic Proteins
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
                                                                                                   APPLICANT:
                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                       4346
                                                                                                                                                                                                                                                                                                              4406 ATAGTGCTTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4166 AGGTTCÀCCTACGACCACGCTGAGCTGGAAAAGGAAAATCGCGTGCTGCTCCCCGCCCCCA 4225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3683 CCAAGATTTGCAGAACTTGTGGAAAAACTAGGTGATTTGCTT---CAAGCAAATGTACAA :739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         213 AsnTyrThrArgIlePheLeuTyrSerGlyGluPro-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LeuGlyAsnGluThrSerValPheGlyProThrGlyAsnLysThrLeuGlyLeuAlaIle 246
                                                                                                                                                                                                                                                                                                                                                        LeuGlnIlePhe 270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGCAGCACTCTGTTGĠĊĊŤĊŤĊĊĊATGCTGAAGCGCTTCÁĊĊŤĠĠACTĠÁĊÁĠĊAAACCC 4045
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MetAlaLysTrpValLysGlnAspAsnGluThrGlyIleTyr-----TyrGlu 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TrpLysGluAsnGlyThrLeuValGlnValAlaThrIleSerGlyAsnMetPheAsnGln 152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTTCTAGAAGCÁĆATGTĠTÁTTTATACĆĆCCAĠĠĀÁĀCTAGCTTŤTĠCCAGTATTATGC 4345
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTCTTCAAGGAAAGTATTTCAGCTCCGAAGTTTAATTCAGGAAGCTCTGATGATGATGAGA 3886
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                 LAHIVE & COCKFIELD
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                                                                        From Ragweed and
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                                                                        Uses
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match:
DB:
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Best Local Similarity:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1349 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: AUGUST 15, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/529,951
FILING DATE: May 29, 1990
APPLICATION NUMBER: US 07/325,365
FILING DATE: March 17, 1989
ATTORNEY/AGENT INFORMATION:
NAME: Amy E. MANDERS: 36,207
REFERENCE/DOCKET NUMBER: IMI-018CN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEPAX: (617)227-5941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION:
148 AsnMetPheAsnGlnMetAlaLysTrpValLysGlnAspAsnGluThrGlyIleTyr---
                                                                                                                                                                                       108 ArgProGluMetAspAlaProPheTrpCysAsnGlpGlyAlaAlaCysPhePheGluGly 127
                                                                                                                                                                                                                                                                                                                                                                                                             586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      526 TGTCCAGGAGGCATGATTAAGTCCCAACGATGGTCCACCAATTTTAAGACAACAAAGTGAT 585
                                                                                                                                                                                                                                                                                                                                                          68 LeuGlyHisLeuLysIleMetHisAspAlaIleGlyPheArgSerThrLeuThrGlyLys 87
                                                                                                                                                                                                                                                                                                                                                                                                                                            48 AspAspIleGluValPheArgLeuGlnAlaProValTrpGluPheLysTyrGlyAspLeu 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              35 Cyspro-----ThrGlySerproIleProValMetGluGlyAsp 47
                                                                GCTGATGACACCCATTATCAAGATAAAGGCATGCTA-----
                                                                                                   IleAspAspValHisTrpLysGluAsnGlyThrLeuValGlnValAlaThrIleSerGly 147
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                                                                                                                                                                                                                                                                                                                                                                                                           GGTGATGCTATAAATGTTGCTGGTAGTTCACAAATATGG--
                                                                                                                                                                                                                                                                                                                     ATCGACCATTGCTCGCTCAGTAAGGCTTCCGATGGGGCTGCTCGATATCACCCTCGGCAGC 684
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Matches:
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PATENT NO. 5699204
GENERAL INFORMATION:
APPLICANT: Rogers, Bruce
APPLICANT: Klapper, David G.
APPLICANT: Klapper, Thorunn
APPLICANT: Kuo, Mei-chang
APPLICATION NUMBER: US 07/529,951
FILING DATE: May 29, 1990
APPLICATION NUMBER: US 07/325,365
FILING DATE: March 17, 1989
ATTORNEY/AGENT INFORMATION:
NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: 1MI-018CN
                                                                                        CURRENT AKEL-
APPLICATION NUMBER: L,
FILING DATE: August 15, 1994
PRIOR APPLICATION DATA: US 07/529,951
**DIICATION NUMBER: US 07/529,951
**DIICATION NUMBER: US 07/725,365
                                                                                                                                                                                     COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/290,448A
                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Kuo, Mei-chang
TITLE OF INVENTION: Allergenic Proteins
NUMBER OF SEQUENCES: 93
                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
                                                                                                                                                                                                                                                                                                                                                               STREET: STREET:
                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 02109-1875
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DB:
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Best Local Similarity:
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TELEPHONE: (617)227-7400
TELEPAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 73:
SEQUENCE CHARACTERISTICS:
LENGTH: 1349 base pairs
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STRANDEDNESS: sing
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                                             SerValPheGlyProThrGly---AsnLysThrLeuGlyLeuAlaIleLysArgPheTyr 250
                                                                                                                                                                                                                                                                                                                  GTCGTTAACAACAACTACGACAGATGGGGAACGTACGCCATCGGTGGTAGCTCGGCCCCA
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Matches:
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Percent Similarity:
Best Local Similarity:
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                                                                                                                                                             US-08-175-069A-73
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US-08-175-069A-73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 73, Application US/08175069A Patent No. 5776761
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION UMBER: US 07/529,951
FILING DATE: May 29, 1990
APPLICATION UMBER: US 07/525,365
FILING DATE: March 17, 1989
ATTORNEY, AGENT INFORMATION:
NAME: Amy E. Mandragouras
REGISTRATION UTMBER: 36,207
REFERENCE/DOCKET NUMBER: IMI-018DV
TELECOMMUNICATION: TREORMATION:
                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (617)227-5941 INFORMATION FOR SEQ ID NO: 73:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATURG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                    MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Rogers, Bruce
APPLICANT: Klapper, David G.
APPLICANT: Rafnar, Thorunn
APPLICANT: Kuo, Mei-chang
TITLE OF INVENTION: Allergenic Proteins
NUMBER OF SEQUENCES: 93
                                                                                                        No.:
                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                     LENGTH: 1349 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                              LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         251 TyrProPheLysProHisLeuProThrLysGluPheLeuLeuSerLeuLeuGlnIlePhe
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60 State Street
                                                                                                                                                                                                                                                       linear
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                   Sequence 73, Application US/08461939B Patent No. 6335019 GENERAL INFORMATION:
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                                                                                                                                                             ThrTyrGluGluIleProLeuProIleArgAsnLysThrLeu 313
                                                                                                                                                                                                        TATAATAATCATAAATACTTATTTTATTTTATT
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Rogers,
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                                                                                                                             CCATTACGTTCAAGTACTCTA 1293
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                                                                                                                                                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-461-939B-73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/464,000
FILING DATE: 05-JUN-1995
APPLICATION NUMBER: US 08/290,448
FILING DATE: 15-AUG-1994
APPLICATION NUMBER: US 07/529,951
FILING DATE: 29-MAY-1990
APPLICATION NUMBER: US 07/325,365
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APPLICANT:
APPLICANT:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 17-MAR-1989
ATTORNEY/AGENT INFORMATION:
NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                     No.:
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                                                                                                                                                                                                                                                                                                                   Match:
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MEDIUM TYPE: Floppy
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CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION: Metho
TITLE OF INVENTION: Prote
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LOCATION:
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          AsnTyrThrMetGluTrpTyrGluLeuPheGlnLeuGlyAsnCysThrPheProHisLeu 107
                                                                                        LeuGlyHisLeuLysIleMetHisAspAlaIleGlyPheArgSerThrLeuThrGlyLys
                                                         ATCGACCATTGCTCGCTCAGTAAGGCTTCCGATĞGGCTGCTCGATATCACCCTCGGCAGC
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Protein Allergen Using Peptides Which Inlcude A T Cell Epitope
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Indels:
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                                                                                                                                                                                                                                                                                                                     Sequence 7:
Patent No.
                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                          APPLICANT: Rogers, Bruce
APPLICANT: Klapper, David G.
APPLICANT: Rafnar, Thorunn
APPLICANT: Kuo, Mei-chang
TITLE OF INVENTION: Allergenic Peptides from Ragweed Pollen
                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                       COUNTRY:
                                                                                                                         STATE:
                                                                                                                                     CITY: Boston
                                                                                                                                                        STREET:
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6335020
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                                                                                                                       Massachusetts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IleAspAspValHisTrpLysGluAsnGlyThrLeuValGlnValAlaThrIleSerGly 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AACATGTTCACCGATCACGTTGACCAAAGAATGCCTAGATGTAGATTTGGGTTTTTTCCAA 855
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                                                                                                                                                      60 State Street
                                                                                                                                                                    LAHIVE & COCKFIELD,
                                                                                                                                                                                                      93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --PheGluTyrTrpPheLeuProMetLysPheProPheIleLysIle
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      Version
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Alignment Scores:
Pred. No.:
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Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-464-000-73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 73:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 07/529,951
FILING DATE: 29-MAY-1990
APPLICATION NUMBER: US 07/325,365
FILING DATE: 17-MAR-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: cDNA FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: IM.
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/01 FILING DATE: 05-JUN-1995 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    URRENT APPLICATION DATA:
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TYPE: nucleic acid
STRANDEDNESS: single
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                       Thr-
                                                            GTCGTTAACAACTACGACAGATGGGGAACGTACGCCATCGGTGGTAGCTCGGCCCCA 915
                                                                                                                                                                                AsnMetPheAsnGlnMetAlaLysTrpValLysGlnAspAsnGluThrGlyIleTyr--- 166
                                                                                                                                                                                                                             GCTGATGACACCCATTATCAAGATAAAGGCATGCTA----
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15-AUG-1994
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                 -TrpPheAspSerTyrAspCysSerLysPheValLeu 194
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Matches:
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                                                                                                                                                                                                                                                                                                            ----ACCCAACACCAATTTGTATTATTGCTCGGG
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US-08-290-448A-58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 58, Application Patent No. 5676954
                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: AMY E. Mandragouras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: IMI-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227,7400
                                                                             INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/290,448A FILING DATE: AUGUST 15, 1994 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/529,951
                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IHM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Kuo, Me:
TITLE OF INVENTION:
                 LENGTH: 1328 base pairs TYPE: nucleic acid
                                                                                                                                                                                                                                            APPLICATION NUMBER: US
FILING DATE: May 29, 1
APPLICATION NUMBER: US
FILING DATE: March 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET:
STRANDEDNESS:
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ON: Allergenic Proteins From Ragweed
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MOLECULE TYPE:
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---GGAGAAGCCGTTCTAAGACTCACTAGTAGTGCTGGTGTACTCTCATGCCATCAAGGA 1.16
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                                                                                                                               CTCCCATCCGGGTCTGATCCAGTGCTAACCCCTGAGCAA---
                                                                                                                                                              LeuTyrSerGlyGluProThrTyrLeuGlyAsnGluThrSerValPheGlyProThrGly 238
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Best Local Similarity:
Query Match:
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GENERAL INFORMATION:
APPLICANT: Rogers
APPLICANT: Klappe
                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (617)227-5941 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 07/32
FILING DATE: March 17, 1989
ATTORNEY/AGENT INFORMATION:
NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/290,448A FILING DATE: August 15, 1994 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/529,951 FILING DATE: May 29, 1990 APPLICATION NUMBER: US 07/325,365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: INTELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Kuo, Mei-chang
TITLE OF INVENTION: Allergenic Proteins From Ragweed and
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
                                                                                                                                                                                                                                                  FEATURE:
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STREET: Boston
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                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: sing
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Klapper, David (
Rafnar, Thorunn
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-ThrGlySerProIleProValMetGluGlyAsp 47
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RESULT 10
US-08-175-069A-58
                         Sequence 58, Application US/08175069A
Patent No. 5776761
GENERAL INFORMATION:
            APPLICANT:
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          Rogers, Bruce
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US-08-175-069A-58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
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PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 07/529,95
FILING DATE: May 29, 1990
APPLICATION NUMBER: US 07/325,36
FILING DATE: March 17, 1989
ATTORNEY/AGENT INFORMATION:
NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: 36,207
REFERENCE/DOCKET NUMBER: IMI-018
TELECOMMUNICATION INFORMATION:
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INFORMATION FOR SEQ ID NO:
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FEATURE:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ADDRESSEE: LAHIVE & COCKFIELD,
STREET: 60 State Street
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TITLE OF INVENTION: Allergenic
NUMBER OF SEQUENCES: 93
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APPLICATION NUMBER: US
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                                                                                                                                                                                                     68 LeuGlyHisLeuLysIleMetHisAspAlaIleGlyPheArgSerThrLeuThrGlyLys
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Rafnar, Thorunn
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Conservative:
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-ACCCAACACCAATTTGTATTATTGCTCGGG
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RESULT 11
US-08-461-939B-58
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                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Rogers, Bruce
APPLICANT: Klapper, David
APPLICANT: Rafnar, Thorus
APPLICANT: Kuo, Mei-chang
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                     NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSE: LAHIVE & COCKFIELD,
                                                                                                                                                                                                                                APPLICANT: Kuo, Mei-chang
TITLE OF INVENTION: Methods For Treating Sensitivity To A
TITLE OF INVENTION: Protein Allergen Using Peptides Which Inloude A T Cell Epitope
                                                                                                                            STATE: Maria
                                                                                                                                                            STREET:
                                                                                                                     COUNTRY:
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                                                                                                                                    Massachusetts
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                                                                                                                                                                         28 State Street
                                                                                                               USA
                                                                                                                                                                                                                                                                                                    Klapper, David G.
Rafnar, Thorunn
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   Version #1
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Best Local Similarity:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 07/325
APPLICATION NUMBER: US 07/325
FILING DATE: 17-MAR-1989
ATTORNEY/AGENT INFORMATION:
NAME: Amy E. Mandragouras
REGISTRATION UNMBER: 36,207
REFERENCE/DOCKET NUMBER: IMI-
TELECOMMUNICATION INFORMATION:
TELECHHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . No. :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
NIMBER: US/08/461,939B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: single TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
     835 GTCGTTAACAACAACTÁCGACAGATGGGGAACGTACGCCATCGGTGGTAGCTCGGCCCCA 894
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                                                                                                                   AsnMetPheAsnGlnMetAlaLysTrpValLysGlnAspAsnGluThrGlyIleTyr---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGTGATGCTATAAATGTTGCTGGTAGTTCACAAATATGG----
                                                                                                                                                            GCTGATGACACCCATTATCAAGATAAAGGCATGCTA-
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                                                                                                                                                                                                                                                                                                                                           AsnTyrThrMetGluTrpTyrGluLeuPheGlnLeuGlyAsnCysThrPheProHisLeu 107
                                                                                 AACATGTTCACCGATCACGTTGACCAAAGAATGCCTAGATGTAGATTTTGGGTTTTTCCAA
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LICATION NU DATE: DATE: LICON NU DATE: LICON NU DATE: LICON NU DATE: LAGENT I LAGION NU E. LATION NU E. LATION NU LATION NU E.	NUMBER OF SEQUENCE: 93 CORRESPONDENCE ADDRESS: 93 CORRESPONDENCE ADDRESS: ADDRESSE: LAHIVE & COCKFIELD, LLP STREET: 60 State Street CITY: Boston STATE: Massachusetts COUNTRY: USA ZIP: 02109-1875 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION NUMBER: US/08/464,000 FILING DATE: 05-UN-1995	000	1042 239 1081 259 1108 278 1165 288 1225	Qy 182 Thr
Db 955 TTAGCGAGGACTGGTACTGGCAACGCAGAGTCGATGTCGTGAAACAGATAAA 1014 Oy 199 LysLeuAlaGluPheGlyAlaGluPheLysAssnIleGluThrAssnTyrThrArgIlePhe 218	128 IleAspAspValHisTrpLysGluAsnGlyThrLeuValGlnValAlaThrIleSerGly	604 604 88 108	0.143 Length: 1328 89.50 Matches: 68 27: 29.45\$ Conservative: 28 Mismatches: 113 5.09\$ Indels: 117 4 09\$ Gaps: 15 COPY_31_346 (1-316) x US-08-464-000-58 (1-1328) PPro	TELECOMMUNICATION INFORMATION: TELEPHONE: (617)227-7400 TELEPAX: (617)227-7540 INFORMATION FOR SEQ ID NO: 58: SEQUENCE CHARACTERISTICS: LENGTH: 1328 base pairs TYPE: nucleic acid STEANDENNESS: single TOPOLOGY: linear MOLECULE TYPE: CDNA FRANTICN: CDS LAME/KEY: CDS LAME/KEY: CDS LAME/KEY: CDS

ProAspProTyrCysGlnAl ::: :::	Gaps: -316) x US-07-792-600-	th Ger Ger	. 1.37	JERGETH: 4440 base pairs TYPE: NUCLEIC ACID TYPE: STRANDEDNESS: single TOPOLOGY: lines:	I TELEPHONE: (415) 705-8410 I TELEPHONE: (415) 705-8410 I TECRMATION FOR SEQ ID NO: 1: SECURENCE CHARACTERITETICS:			COMPUTER: IBM PC COMPATIBLE COPERATING SYSTEM: PC-DOS/MS-DOS FORWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:	COUNTRY U.S.A. COUNTRY U.S.A. ZIP: 94104 COMPUTER REALBABLE FORM: MEDIUM TYPE: Electrication	ADDRESSEE: Peter G. Carroll FIRET: 220 Montgomery Street, Suite 710 CITY: San Francisco CITY: San Francisco CITY: San Francisco	TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: TEMPLATE-DEPENDENT ENZYMATIC SYNTHESIS OF NUCLEIC ACID NUMBER OF SEQUENCES: 34 CORRESPONDENCES: 34	1. Application 03/0//3 0. 6008045 INFORMATION: CANT: COPPLAND, WILLIA CANT: WANG TERROS		Qy 308 IlearqAsnLysThrLeu 313 :: ::: ::: ::: ::: ::: ::: ::::	1225 TATTTTATTCCA	QY 288 TrpPheLeuProMetLysPheProPheIleLysIleThrTyrGluGluIleProLeuPro 307	278	Db 1108GGAGAAGCCGTTCTAAGACTCACTAGTAGTGCTGGTGTACTCTCATGCCATCAAGGA 1164	1081
RESULT 14 US-09-157-021-1 ; Sequence 1, Application US/09157021A	1412 CAAGATTTGAAAGGAGAAACTTTTTCT	Oy 290 LeuproMetLysPheProPhelleLysIleThrTyrGlu	270 1304	Qy 250 TyrTyrProPheLysProHisLeuProThrLysGluPheLeuLeuSerLeuLeuGlnIle 269	Qy 231 ThrSerValPheGlyProThrGlyAsnLysThrLeuGlyLeuAlaIleLysArgPhe 249 ::::	Qy 211 GluThrAsnTyrThrArgIlePheLeuTyrSerGlyGluProThrTyrLeuGlyAsnGlu 230	Qy 199 LysLeuAlaGluPheGlyAlaGlu	Qy 183TrpPheAspSerTyrAspCysSerLysPheValLeuArgThrPheAsn 198	Qy 172 Vally8AlaSerProGluLy8GlyAlaGluThr	Qy 153 MetAlaLysTrpValLysGlnAspAsnGluThrGlyIleTyrTyrGluThrTrpAsn 171	QY 136 ABnGlyThrLeuValGlnValAlaThrIleSerGlyAsnMetPheAsnGln 152 :::	Qy 116 TrpCysAsnGlnGlyAlaAlaCysPhePheGluGlyIleAspAspValHisTrpLysGlu 135	Db 803 GTGGACCTGGAGCCTATGGCTGCCAAGGCT 832	779	Oy 76 AspAlaIleGlyPheArgSerThrLeuThrGlyLysAsnTyrThrMetGluTrpTyrGlu 95	56	Φ.		Db 563 AAGAAAAGATCCATTGGAGCTTCACCGAATCCTTTCTCTGTGCACCACCGCCACGGCAGTT 622 Qy 36 ProThrGlySerProIlePro 42

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Best Local Similarity:
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SEQ ID NO 1
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CURRENT APPLICATION NUMBER: US/09/157,021A
CURRENT FILING DATE: 1998-09-18
EARLIER APPLICATION NUMBER: 07/792,600
EARLIER FILING DATE: 1991-11-15
NUMBER OF SEQ ID NOS: 35
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TYPE: DNA
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                               1046 TATTGGTTGGATGCTTATGAGGATCAGTACAACCAACCAGGTGTGGTATTTCTGTTTGGG 1:05
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 LysLeuAlaGluPheGlyAlaGlu--
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                                                             ---TrpPheAspSerTyrAsp--
                                                                                            GTGGATTCCAGTCACCTCCCATTGGTAAAAGGGGCAGATGAGGAACAAGTATTCCACTTT 1)45
                                                                                                                          ValLysAlaSerPro-----GluLysGlyAlaGluThr---
                                                                                                                                                                                         MetAlaLysTrp---ValLysGlnAspAsnGluThrGlyIleTyrTyrGluThrTrpAsn 171
                                                                                                                                                                                                                        GATTCTGGGAAAGGGACCGTG------TCCTACTTAGGAAGTTTTCTCCCGGAT 925
                                                                                                                                                                                                                                                      Asn-----GlyThrLeuValGlnValAlaThrIleSerGlyAsnMetPheAsnGln 152
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APPLICANT: Wang, Teresa S. F.
APPLICANT: Wang, Teresa S. F.
FITTLE OF INVENTION: Drug Screening
FILE REFERENCE: STDU-03485
CURRENT APPLICATION NUMBER: US/09/156,842A
CURRENT FILING DATE: 1998-09-18
EARLIER APPLICATION NUMBER: 07/792,600
EARLIER FILING DATE: 1991-11-15
NUMBER OF SEQ ID NOS: 35
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56 GlnAlaProValTrpGluPheLysTyrGlyAspLeuLeuGlyHisLeuLysIleMetHis 75
                                                                                                                                                                                                                                                                                                                                            16 LysArgPheAspPheArgProLysProAspProTyrCysGlnAlaLysTyrThrPheCys 35
                                                                                                                   ValMetGluGlyAsp------AspAspIleGluVal----
                                                                                                                                                                            CCTTCAGGAAAAATTGCTTCCCCTGTCTCCAGAAAGGAGCCTCCATTAACTCCTGTTCCT 682
                                                              CTTAAACGTGCTGAATTTGCTGGCGATGATGTACAGGTCGAGAGTACAGAAGAAGAGCAG
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Search completed: April 25, 2004, 05:51:01 Job time : 140.894 secs	Qy 306 LeuProIleArgAsnLysThrLeuSer 314	290 LeuProMetLysPheProPheIleLysIleThrTyrGlu	_	1256	1196	1166	Db 1106 AAAGTTTGGATTGAATCAGCCGAGACCCCATGTGAGCTGTTGTGTCATGGTGAAAAATATGC Qy 211 GluThrAsnTyrThrArgIlePheLeuTyrSerGlyGluProThrTyrLeuGlyAsnGlu	199	1046 TATIGGTTGGATGCTTATGAGGATCAGTA	183	986 GIGGATICCAGTCACCTCCCAT	172	926 GTCTCTTGTTGGGA	153 MetAlaLysTroValLysGlnAsnAsn	::: 878 GATTCTGGGAAA	Qy 136 AsnGlyThrLeuValGlnValAlaThrIleSerGlyAsnMetPheAsnGln	Db 833 TGGGACAAAGAGAGTGAGCCAGCAGCAGGAAGAAGTGAAAACAAGAGGCG	116 TrpCysAsnGlnGlyAlaAlaCysPhePheGluGlyIle	Db 803 GTGGACCTGGAGCCTATGGCTGCCAAGGCT	96 L	Db 779GATGAGCCCATGGAAGTTGAAGAG	Qy 76 AspAlaIleGlyPheArgSerThrLeuThrGlyLyBAsnTyrThrMetGluTrpTyrGlu
		GluIlePro 305 ::::: AAATGCCACAGCTTCCT :.411	nPheGluTyrTrpPhe 289	LeuGInIle			rcarggrgaaaaataic :1165 hrTyrLeuGlyAsnGlu :230	PheLysAsnIle 210			AACAAGTATTCCACTTT :L045					lyAsnMetPheAsnGln 152	:: %AGTGAAACAAGAGGCG 877	spValHisTrpLysGlu 135	ATGGCTGCCAAGGCT 332	luMetAspAlaProPhe :115	CCATGGAAGTTGAAGAG 302	

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Result
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-MODEL-frame+ p2n.model -DEV=xlh
-C-pCgn2_1/USFTO_spool/US10010050/runat_22042004_113203_27539/app_query.fasta_1.1372
-Q-pCgn2_1/USFTO_spool/US10010050/runat_22042004_113203_27539/app_query.fasta_1.1372
-DB=N Geneseq_29Jan04 -QFMT=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEARSIZE=500 -MINLEN=000000000
-USER=US10010050 @CGN 1 1819 @runat 22042004 113203 27539 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG
-USER=US100101050 @CGN 1 TIMEOUT=30 -THREADS=1 -XGAPDP=10 -XGAPDEXT=0.5 -FGAPOP=6
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Maximum Match 100%
Listing first 45 summaries
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AAX02855 standard; DNA; 1486 BP (first

AAX02855;

RESULT 1 AAX02855

ALIGNMENTS

Secreted protein; zsig46; human; chromosome 13; thyroid; disease; hypothyroidism; Graves' disease; thyrotoxicosis; thyroid cancer; Hirschsprung's disease; neuronal ceroid-lipofucinosis; Wilson dis Reiger syndrome; immunoassay; detection; anti-idiotypic antibody; therapy; diagnostic; ss. disease;

Human zsig46 14-MAY-1999

DNA.

Homo sapiens

PA	X	PR	X	קי	×	Дď	×	PN	×	ΉŢ	ΉŢ	ΗŢ	FH	×
(ZYMO) ZYMOGENETICS INC.		24-JUL-1997;		24-JUL-1998;		04-FEB-1999.		WO9905275-A1.				CDS	Key	
ETICS INC.		97US-0053613P.		98WO-US015431.						/product= "zsig46"	/*tag= a	471087	Location/Qualifiers	

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left Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1751 BP;
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, Endress GA,
               GlnValAlaThrIleSerGlyAsnMetPheAsnGlnMetAlaLysTrpValLysGlnAsp
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11-JAN-2000; 2000JP-00118774
02-MAY-2000; 2000JP-00183765
                                     Claim
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The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isoland nucleotide sequences of 5'- and 3'-ends of the cDNA molecules.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a full length human cDNA of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from EPO
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                                                                                                         This invention describes the isolation of a novel human secreted protein, consig46 encoded by a gene on chromosome 13 which is mainly expressed in the thyroid. This product can be used to study secretion of proteins from cells and also to treat or prevent deficient expression of zeig46, which considered with thyroid diseases (e.g. hypothyroidism, Graves' considered with thyroid diseases (e.g. hypothyroidism, Graves' considered with thyroid cancer etc.) or with diseases that cinvolve genes in the same region of chromosome 13 (e.g. Hirschsprung's considered considered cancer and sease and Reiger considered cons
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New secreted polypeptide, zsig46, and its fragments, related fusion proteins - used for diagnosis and treatment of thyroid disorders or
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The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence was used as the representative sequence from a human clone which was used in homology searches to identify the clone. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from
                                                                                                                                                                                                                                                                                                                                                             08-JUL-1999; 99JP-00194486
11-JAN-2000; 2000JP-00118774
02-MAY-2000; 2000JP-00183765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo
 Sequence 697
                                                                                                                                                                                                    Example 11; SEQ ID NO 1884; 1380pp + Sequence Listing;
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                                                                                                                                                                                                                                                                                                Wakamatsu A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; full length cDNA; cDNA synthesis; oligo-capping;
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S, Otsuki
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Alignment Scores: 1.9e-91 Length: 697
Pred. No.: 896.00 Matches: 170
Score: 896.00 Conservative: 3
Best Local Similarity: 90.91% Mismatches: 8
Query Match: 50.97% Indels: 6
DB: Gaps: 2
US-10-010-050A-2_COPY_31_346 (1-316) x AAK93424 (1-697)

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ATCCCAGTTATGGAGGGTGATGATGACACTGAAGTTTTTCGATTACAAGCCCCCAGTATGG

321

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The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is the nucleotide sequence of the 5'-end of
                                                                                                                                                                                                                                                                                                                         08-JUL-1999;
11-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human cDNA 5'-end sequence, SEQ ID NO: 618.
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              a cDNA provided in the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from EPO
                                    Homo sapiens.
                                                             cervical
                                                                       Probe; human; microarray;
                                                                                                Probe #15029
                                                                                                                         12-OCT-2001
                                                                                                                                                AAI25096;
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                                                             cancer;
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03-AUG-2000;
21-SEP-2000;
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26-MAY-2000;
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              IleValHisLysGlnPheTyrLeuPheTyrAsnPheGluTyrTrpPheLeuProMetLys
                                                                LysProHisLeuProThrLysGluPheLeuLeuSerLeuLeuGlnIlePheAspAlaVal
                                                                                                                                                                                                               LeuArgThrPheAsnLygLeuAlaGluPheGlyAlaGluPheLygAsnIleGluThrAsn
                                                                                                                                                                                                                                                                                                    GCAAAGTGGGTGAAACAGGACAATGAAACAGGAATTTATTATGAGACATGGAATGTAAAA
                                                                                                 TTTGGGCCAACAGGAAACAAGACTCTTGGTTTAGCCCATAAAAAGATTTTATTACCCCCTTC
                                                                                                                  PheGlyProThrGlyAsnLysThrLeuGlyLeuAlaIleLysArgPheTyrTyrProPhe
                                                                                                                                                   TATACAAGAATATTTCTTTACAGTGGAGAACCTACTTATCTGGGAAATGAAACATCTGTT
                                                                                                                                                                         TyrThrArgIlePheLeuTyrSerGlyGluProThrTyrLeuGlyAsnGluThrSerVal
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; 2000US-00632366.
; 2000US-0234687P.
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8 8

154 AlaLysTrpValLysGlnAspAsnGluThrGlyIleTyrTyrGluThrTrpAsnValLys

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US-10-010-050A-2_COPY_31_346 (1-316)

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Best Local
Query Match
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ABA70786
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30-JUN-2000; 2000US-0060840B.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-02346559P.
04-OCT-2000; 2000GB-00024263.
                                                                                                                         The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                            gene
                                                                                                                                                                                                                     Claim
                                                                                                                                                                                                                                                                               WPI; 2001-483447/52.
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              Match:
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                                                                                                                                                                                                                                                      genome-derived single
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26-MAY-2000;
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                                                                                          genome-derived single exon nucleic expression in human placenta.
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2000US-0207456P.
; 2000US-0060840B.
; 2000US-00632366.
; 2000US-0234687P.
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09-AUG-2001.

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                                                                                                                                                                              Human; gene expression; heart; microarray; vascular system; cardiovascular disease; hypertension; cardiac arrhythmia; congenital heart disease; ss.
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     measuring human gene expression in a sample derived from human heart. The present sequence is one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity:
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27-SEP-2000;
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2000US-00608408
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RESULT 11

ARK44992
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Query Match:
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26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
21-SBP-2000; 2000US-0234687P.
27-SBP-2000; 2000US-0234585P.
04-OCT-2000; 2000GB-00024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is one of the probes of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene
                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human genome-derived single exon nucleic acid probes useful for analyzing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 4; SEQ ID NO 19549; 658pp + Sequence Listing;
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AlaSerProGluLysGlyAlaGluThrTrpPheAspSerTyrAspCysSerLysPheVal
                                                                                                      AlaLysTrpValLysGlnAspAsnGluThrGlyIleTyrTyrGluThrTrpAsnValLys
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cancer; leukaemia; lymphoma; myeloma; ss.
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26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-0060840B.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
04-OCT-2000; 2000GB-00024263.
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The present : probes which
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21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    measuring human gene expression in a sample derived from human adult liver, comprising one of 13109 defined nucleotide sequences given in the specification (or complements) fragments). The probe hybridises at high stringency to a nucleic acid molecule expressed in the human adult liver. (1) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be involved in genetic liver diseases such as cirrhosis, hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is associated with coronary heart disease. ABS25011-ABS51005 represent human liver single exon nucleic acid probes of the invention. Note: The sequence information for this patent does not appear in the printed sequence information for this patent does not appear in the printed sequence information for this patent does not appear in the printed sequence.
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ftp.wipo.int/pub/published_pct_sequences
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30-JUN-2000;
03-AUG-2000;
                       The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human lung comprising single exon nucleic acid probes having one of 12614 nucleic acid sequences mentioned in the specification, or their complements or the 12387 open reading frames derived from the 12614 probes. Also included are a microarray comprising the novel set of probes; the novel set of probes which hybridise at high stringency to a nucleic acid expressed in the human lung; measuring gene expression in a sample derived from human lung, comprising (a) contacting the array with a collection of detectably labeled nucleic acids derived from human lung man, and (b) measuring the label detectably bound to each probe of the array; identifying exons in a enkaryotic genome, comprising (a) algorithmically predicting at least one con from genomic sequences of the array and (b) producting at least one con from genomic sequences of the context 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     chronic obstructive pulmonary disease; interstitial lung disease; familial idiopathic pulmonary fibrosis; neurofibromatosis; tuberous sclerosis; Gaucher's disease; Niemann-Pick disease; thermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis; pulmonary histiocytosis; lymphangioletiomyomtosis; karagener syndrome; pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia; primary ciliary dyskinesis; pulmonary hypertension;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Spatially-addressable set of single exon nucleic acid probes, used measure gene expression in human lung samples.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CC comprising (a) identifying exons from genomic sequence by the method CC above and (b) measuring the expression of each of the exons in several CC tissues and/or cell types using hybridisation to a single exon CC microarrays having a probe with the exon, where a common pattern of CC microarrays having a probe with the exon, where a common pattern of CC the exons should be assigned to a single gene; a peptide comprising one CC of 12011 sequences, mentioned in the specification, or encoded by the CC probes/open reading frames (ORF). The probes are used for gene expression CC analysis, and for the study of lung diseases such as asthma, lung CC disease (IID), familial idiopathic pulmonary disease (OCD), interstitial lung CC disease (IID), familial idiopathic pulmonary fibrosis, neurofibromatosis, CC tuberous sclerosis, Gaucher's disease, Niemann-pick disease, Hermansky-CC histiocytosis, lymphangioleiomyomtosis, pulmonary alveolar proteinosis, CC dyskinesis, pulmonary hypertension and hyaline membrane disease. The CC invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp. wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            labeled nucleic acids from eukaryote lung mRNA, to a single exon probe, having a fragment identical to the predicted exon, the probe is included in the above mentioned microarray; assigning exons to a single gene,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 494
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                                              SerGlyLeu 316
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                                                                                                                                                                                                                                                                                                                   treating, preventing or ameliorating medical conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional activity, immune stimulating or suppressing activity, haematopoisesis regulating activity, tissue growth activity, haemostatic activiny inhibin activity, chemotatic/chemokinetic activity, haemostatic and thrombolytic activity, receptor/ligand activity, anti-inflammatory activity, cadherin/tumour invasion suppressor activity, tumour inhibition activity. The EST sequences are also stated to be useful for gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New polynucleotides encoding human secreted
human blood, kidney, foetal lung, placenta,
pituitary, retina and colon cDNA libraries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Expressed sequence tag; secreted protein; haematopoiesis regulator; tissue growth; activin; inhibin; tumour invasion suppressor; EST; human; chemotaxis; chemokinesis; haemostasis; gene therapy; thrombolysis;
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                                                                                                      121 AlaAlaCysPhePheGluGlyIleAspAspValHisTrpLysGluAsnGlyThrLeuVal
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                                             | GlnValAlaThrIleSerGlyAsnMetPheAsnGlnMetAlaLysTrpValLysGlnAsp
AsnGluThrGlyIleTyrTyrGluThrTrpAsnValLysAlaSerProGluLysGlyAla 180
                                                                                     CAAGTAGCAACTATATCAGGAAACATGTTCAACCAAATGGCAAAGTGGGTGAAACAGGAC
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241 ThrLeuGlyLeuAlaIleLysArgPheTyrTyrProPhe 253	221 SerGlyGluProThrTyrLeuGlyAsnGluThrSerValPheGlyProThrGlyAsnLys 240	201 AlaGluPheGlyAlaGluPheLyBAsnIleGluThrAsnTyrThrArgIlePheLeuTyr 2:0	181 GluThrTTpPheAspSerTyrAspCysSerLysPheValLeuArgThrPheAsnLysLeu 200	

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

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Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh
-MODEL=frame+ p2n.model -DEV=xlh
-Q=/cgn2 _1/USETO _Spool/US10101050/runat _22042004 _113204 _27556/app_query.fasta_1.1372
-Q=/cgn2 _1/USETO _Spool/US101010050/runat _22042004 _113204 _27556/app_query.fasta_1.1372
-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPELT=0 -LOOPEXT=0
-UNITS=bùts -START=1 -END=-1 -MARIX=blosum62 -TRANS=human40.cdi -LIST=45
-DCCALIGN=200 -THR _SCORE=pct -THR_MAX=1100 -THR _MIN=0 -ALIGN=15 -MODE=LOCAL
-DUTFMT=pto -NORM=ext -HBAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10010050 @CGN 1 1 6283 @runat _22042004 113204 _27556 -NCPU=6 -ICPU=3
-NO _MMAP -LARGEQÜERY -NEG_SCORES=0 -MAIT -DEPBIOCK=100 -LONGLOG
-DEV_TIMEDUT=120 -MARN_TIMEDUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

AUZ80382 AUZ80382 NIESE2 Homo sapiens cDNA clone NIESE2001763 5', mRNA seguence. AUZ80382 AUZ80382 AUZ80382:1 GI:2829609 EST. Homo sapiens (human) Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Genome Research Center
Korea Research Institute of
52 Eoeun-dong Yuseong-gu,
Tel: +82-42-860-4470
Fax: +82-42-860-4409
                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 607)

Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: genomics@hri.co.jp

HRI human cDNA Project, Sugiyama, T.; Wakamatsu, A.; Irie, R.;

Umczawa, A.; Fukuma, M.; Kusakari, S.; Hata, J.; Ishii, S.; Yamamoto, J.;

Isono, Y.; Saito, K.; Nakamura, Y.; Masuho, Y.; Nagai, K.; Isogai, T.

HRI human cDNA project; cDNA library construction & 5'-end one
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Isogai,T., Hata,J., Tomoya,Y. and Umezawa,A.
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                                                                                           Contact: Kim YS
                                                                                                                                Kim, Y.S.
21C Frontier Korean EST
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                                                                                                                                                                                                                                                                                                                                                                     mRNA sequence.
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81-438-52-3975
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/mol_type="mRNA"
/db_xref="taxon:9606"
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/clone_lib="N1ESE2"
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BQ417448
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Location/Qualifiers
             Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K., Lemishka,I., Scearce,M., Brestelli,J., Gradwohl,G., Clifton,S., Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A., Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R., Williams,T., Jackson,Y. and Bowers,Y. Endocrine Pancreas Consortium Unpublished (2000)
Other ESTs: ix38b05.xl Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue Contact:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BQ417448
623 bp mRNA linear EST 15-JUL-200: ik38b05.yl HR85 islet Homo sapiens cDNA clone IMAGE:5783001 5' similar to SW:CLN5_HUMAN 075503 CLN5 PROTEIN. [1] ;, mRNA sequence
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Plate: 67 row: D column: 07
                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
Endocrine Pancreas Consortium
                                                                                                                                                                                                                                                                                                                      Mammalia;
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//Clone lib="SIRMS5"
//Clone lib="SIRMS5"
//Clone lib="SIRMS5"
//Clone Prector; pCNS; Site 1: ECORI; Site 2: NotI; The poly
//Clone Prector; pCNS; Site 1: ECORI; Site 2: NotI; The poly
//Clone Prector; pCNS; Site 1: ECORI; Site 2: NotI; The poly
(A) + RNA was dephosphorylated with bacco acid
pyrophosphatase (BAP) and then decapped intact mRNA was
ligated with DNA-RNA linker including ECOR I site by
treatment of TA RNA ligase and the first strand CDNA was
synthesized from oligo dT-selected mRNA by priming with
dT-tailed vector. The dT-tailed vector was adjusted to
have about 60nt. The cDNA vector was circularized with E.
coli DNA ligase after digestion of ECORI which site is
also included in vector. An RNA strand converted to a DNA
strand by Okayama-Berg method. The obtained cDNA vectors
were used for transformation of competent cells E. coli
Top10F' by electroporation method. The cDNA libraries
constructed by this method are full-length enriched cDNA
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/cell_line="KMS-5"
/lab_host="Top10F'"
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'db_xref="taxon:9606"
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_line="KMS-5"
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24
Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom.; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 676)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                       BG820113 676 bp mRNA linear EST 22-MAY-2
                                                                                                                                                                                                                                                                                                                 Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                 5', mRNA sequence.
BG820113
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seq primer: -40RP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     obtaining a clone please contact: Dr. Hiroshi Incue (hinoue@im.wustl.edu)
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/clone_lib="HRB5 islet"
/clone_lib="HRB5 islet"
/clone_lib="HRB5 islet"
/nott="Forgan: Pancreas; Vector: pBluescript SK(-); Sit=1:
/nott: Site_2: XhoI; cDNA made by oligo-dT priming.
Size-selected on agarose gel. Average insert size ~1kb. 5'
XhoI site was destroyed after directional cloning.
Amplified once. Contact information: Hiroshi Inoue, MD,
Metabolism Div. (Alan Permutt Lab), Washington University
School of Medicine, Box 8127, 660 South Euclid Ave., St.
Louis, MO 63110, E-mail: hinoue@ingate.wustl.edu, Tel:
314-362-1916, Fax: 314-747-2692."
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/mol_type="mRNA"
/db_xref="taxon:9606"
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Best Local Similarity:
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 787)
                                                                                                                                                                            found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM11253 row: n column: 06
                                                                                                                                                                                                                                                                                                               Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                        NIH-MGC http://mgc.nci.nih.gov/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mRNA sequence.
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CDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information
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/clone lib="NCI CGAP Brn67"
/note="Organ: brain, Vector: pCMV-SPORT6; Site_1: Not Site_2: Sall; Cloned unidirectionally. Primer: Oligo Site_2: Sall; Cloned unidirectionally. Difference insert size 2.3 kb. Constructed by Life Technologic Technologic Page 1.5 kb. Constructed by Life
/clone="IMAGE:5105093"
/tissue_type="cervical carcinoma cell line"
/lab_host="DH10B"
                                                            /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                            /organism="Homo sapiens"
/mol_type="mRNA"
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/db_xref="taxon:9606"
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RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tissue Procurement: Dr. James R. Lupski
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BQ719074 847 bp mRNA linear EST 16-JUL-2002 AGENCOURT 8103813 Lupski_sympathetic_trunk Homo sapiens cDNA clone IMAGE:6191057 5', mRNA sequence.
BQ719074 BQ719074.1 GI:21857971 EST.
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM13590 row: n column: 18
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                                                                                                                                                                                                                                                                                                                                                                                                             quality sequence stop: 484.
Location/Qualifiers
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/note="Organ: cervix; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.4 kb. Library prepared by Life Technologies."
                                                                                   /clone lib="Lupski sympathetic_trunk"
/note="Vector: pcMV-SPORT6 (Life Technologies); Site_1:
NotI; Site_2: SalI; cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:
5'-TCGACCCACGCGTCCG-3' and
5'-GACTAGTTCTAGATCGCGAGCGGCCGCCT(15)-3'. Size selected
1 kb for average insert length 1.9 kb. This is a primary library, non-amplified. Library constructed by Life Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine); available through Life
                                                                                                                                                                                                             /tissue_type="sympathetic trunk"
/dev_stage="adult, 16 yr"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/mol_type="mRNA"
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/clone="IMAGE:6191057"
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NHH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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1 MetArgArgGlyAlaGlyAlaAlaArgGlyArgAlaSerTrpCysTrpAlaLeuAlaLeu
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/note="Organ: cervix; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT
Average insert size 1.5 kb. Library prepared by Life
Technologies."
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/clone="IMAGE:4996891"
/cell line="MGC36"
/lab host="DH10B"
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mol_type="mRNA"
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cgi-bin/cluster.cgi?seq=CSDDB009AB01QP1&cluster=7238.f. Contact regi-bin/gluster.filangelifetech.com URL:
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600 Faraday Avenue Genoscope sequence ID: CSODB009AB01QP1.
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Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7238.f For
more information about this cluster, see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001)
                          BF982158
602308976F1 NIH_MGC_88
BF982158
               mRNA sequence.
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                                      Eukaryota; Metazoa; Chordata; Craniata; Verti Mammalia; Eutheria; Primates; Catarrhini; Hor 1 (bases 1 to 1201)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization Unpublished (2001)
                                                                                                                                                                                                                                                                                   1201 bp mRNA linear EST 31-MAY-2003
AL546472 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CSODIO30YJ01 5-PRIME, mRNA sequence.
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Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
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National Institutes of Health, Mammalian Gene Collection (MGC)
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On Reb 15, 2001 this sequence version replaced gi:12879620. Contact: Genoscope
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/clone lib="NIH_MCC_BS"
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Site 1: NotI, Site 2: Sall; Cloned unidirectionally;
oligo-dT primed. Average insert size 1.767 kb. Library
enriched for full-length clones and constructed by Life
Technologies. Note: this is a NIH_MGC Library."
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/db_xref="taxon:9606"
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                                                                Email: cgapbs r@mail.nih.gov

Tissue Procurement: Dr. James R. Lupski
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM1577 row: g column: 04
High quality sequence start: 7
High quality sequence stop: 277.
Location/Qualifiers
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BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7238.f For
more information about this cluster, see
                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
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National Institutes of Health, Mammalian
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/note="Ist strand cDNA was primed with a NotI-cligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and Ecof. V
sites of the pCMVSPORT 6 vector. Library was normalized."
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/db_xref="taxon:9606"
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                                                                                                                                      Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Kristi A. Egland, Ira Pastan
cDNA Library Preparation: Invitrogen Corp
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLNM14279 row: j column: 21
High quality sequence stop: 637.
                                                                                                                                                                                                                                                                                                                                                                         NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mRNA sequence
CA488543
                                                                                                                                                                                                                                                                                                                                                                                                                                    Mammalia; Eutheria;
1 (bases 1 to 924)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5'-GACTAGTTCTAGATCGCGAGCGGCCCT(15)-3'. Size selected :
1 kb for average insert length 1.7 kb. This is a primary
1 library, non-amplified. Library constructed by Life
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
College of Medicine) and is available through Life
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="Lupski dorsal_root_ganglion"
/note="Vector: pCMV-SPORT6 (Life Technologies); Sit
Not1; Site 2: Sal1; cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:
5'-TCGACCCACGGGTCCG-3' and
                 /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6720309"
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/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                            organism="Homo sapiens"
                                                                                                                       ocation/Qualifiers
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/dev_stage="adult, 36 yr"
/lab_host="DH10B"
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_line="ZR-75-1, MCF7, SK-BR-3, MDA-MB-231,
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Matches:
Conservative:
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1X342662
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lest Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7238.f For
more information about this cluster, see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MetArgArgGlyAlaGlyAlaAlaArgGlyArgAlaSerTrpCyeTrpAlaLeuAlaLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Genoscope
Genoscope - Centre National de Sequencage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 1077)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDMA libraries and normalization
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BX342662 1077 bp mRNA linear EST 02-MAY-2003 BX342662 Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED HOMO sapiens CDNA clone CSODLO04YP03 5-PRIME, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                          http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODL004CH02QPl&cluster=7238.f.
Feng Liang Email : fliang@lifetech.com URL :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BP 191 91006 EVRY cedex - France
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                              Avenue Genoscope sequence ID : CSODL004CH02QP1.
Location/Qualifiers
primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone lib="MARCL"
/note="Vector: pCMV-SPORT6; Site_1: EcoRV; Site_2: Not :;
Subtracted with brain, liver, lung, kidney and muscle.
Directionally cloned. Priming method: oligo-dT. Average insert size: 1800 bp. Library amplification: 26,000 fold.
Kristi A. Egland, James J. Vincent, Robert Strausberg, Bungkook Lee & ITR Pastan: Discovery of new breast cancer genes encoding membrane and secreted proteins.
Manuscript submitted."
                                                                                                                      25-NORMALIZED"
                                                                                       /note="1st strand cDNA was primed with a NotI-oligo(dT)
                                                                                                                                          /clone="CSODLO04YP03"
/cell_type="B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED"
/cell_line="RAMOS CELL LINE"
/clone_lib="Homo sapiens B CELLS (RAMOS CELL LINE) COT
                                                                                                                                                                                                                                                                                  organism="Homo sapiens"
|mol_type="mRNA"
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/lab_host="EMDH108"
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1 (bases 1 to 589)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      found through the I.M.A.G.E. Consortium/LLML at: http://image.llnl.gov Plate: LLCM1172 row: i column: 22 High quality sequence stop: 586.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MetArgArgGlyAlaGlyAla-AlaArgGlyArgAlaSerTrpCysTrpAlaLeuAlaLe 20
                                                                                                                                                                                           /tissue_type="melanotic melanoma, high MDR"
/lab host="DH10B (T1 phage-resistant)"
/clore lib="NIH MGC 62"
/clore lib="NIH MGC 62"
/note="Torgan: skin; Vector: pDNR-LIB (Clontech); Site_1:
/note="Torgan: skin; Vector: pDNR-LIB (Clontech); Site_1:
/note="Torgan: skin; Vector: pDNR-LIB (Clontech); Site_1:
// Stil (ggccgtattaggcc);
Site_2: Stil (ggccattatggcc);
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// adaptors were us
                                                                                                   full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."
                                                                                                                                                                        contained inserts by PCR. This library was enriched for
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/mol_type="mRNA"
/db_xref="taxon:9606"
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AUTHORS
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VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21 LeuTrpLeuAlaValValProGlyTrpSer 30
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CA397574
CA397574.1 GI:24735005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Section on Molecular Structure and Function National Eye Institute 6/331, NIH, Bethesda, MD 20892-2740, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wistow,G., Bernstein,S.L., Wyatt,M.K., Farris,R.N., Behal,A., Touchman,J.W., Bouffard,G., Smith,D. and Peterson,K. Expressed sequence tag analysis of human RPE/choroid for the NEIBank Project: Over 6000 non-redundant transcripts, novel genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 555)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: graeme@helix.nih.gov
Plate: 92 row: h column: 10
Seq primer: M13RP1 reverse primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 301 402 3452
Fax: 301 496 0078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and splice variants Mol. Vis. 8 (4), 20
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                                                                               /clone lib="Human Retinal pigment epithelium/choroid cINA (Un-normalized, unamplified): cg"
/note="Organ: Eye; Vector: pcMVSPORT6; Two different dcnor eyes (75-80 years old) yielded approximately 600 mg of dissected RPE/choroid tissue. This in turn yielded 34C ug of total RNA and 7 ug of mRNA. A directionally cloned cDNA library in the pcMVSPORT6 vector was constructed at Life Technologies (Rockville, MD; now part of Invitrogen Corp), essentially following the protocols of the SuperScript Plasmid System (Invitrogen Corp. chttp://www.invitrogen.com/>). The library code designation was cs. For this library, cDNA inserts were cloned into the NotI/Mull sites of the vector. EST analysis was performed on the unamplified library at the NIH Intramural Sequencing Center (NISC)."
                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="RPE/choroid"
/dev_stage="Adult"
/lab_host="EMDH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="mkNA"
/db_xref="taxon:9606"
/clone="cs92h10"
/clone="cs92h10"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Homo sapiens"
/mol_type="mRNA"
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epithelium/choroid cDNA
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Percent Similarity:
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Command line parameters:

MODEL=frame+ p2n.model -DEV=xlh
-Q-/cgp2_1/USPTO_gpool/US10010050/runat_22042004_113205_27584/app_query.fasta_1.1372
-Q-/cgp2_1/USPTO_gpool/US1001001050/runat_22042004_113205_27584/app_query.fasta_1.1372
-DB=Published_applications_NA -QFMT=fastap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=humman40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXIEN=2000000000 -USER=US10011050_GCGN 11 776_@runat_22042004_113205_27584
-NCPU=6 -ICPU=3 -NO_MAPA -LARGEQUERY -NEG_SCORES=0 -WART -DSPBLOCK=100
-LONGLOG -DEV_INEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
                 10:
11:
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1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB_seq:*
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1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
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7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
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Listing first 45 summaries
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Result

Score

Query Match Length DB

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Description

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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		Sequence 1, Appli Sequence 26, Appl Sequence 28, Appl Sequence 21, Appl Sequence 21716, Sequence 241716, Sequence 21990, A Sequence 11990, A Sequence 11990, A Sequence 11895, A Sequence 21894, Appl Sequence 20677, Appl Sequence 20677, Appl Sequence 14, Appl Sequence 14, Appli Sequence 181138, Sequence 181138, Sequence 181139, Sequence 181139, Sequence 181139, Sequence 10126, Appli Sequence 10787, Appli Sequence 1708, Appli Sequence 1708, Appli Sequence 1708, Appli Sequence 1708, Appli Sequence 103173, Sequence 103173, Sequence 105173, Sequence 105173, Sequence 105173, Sequence 1060, Appli Sequence 10708, Appli Sequence 10708, Appli Sequence 10708, Appli Sequence 10708, Appli Sequence 10708, Appli Sequence 10708, Appli Sequence 5227, Appli Sequence 55, Appli Sequence 65, Appli Sequence 2394, App Sequence 2394, App Sequence 2394, App Sequence 219, App Sequence 2394, App Sequence 219, App	emience 1

US-09-122-383-1

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GENERAL INFORMATION:

APPLICANT: Sheppard, Paul O.

APPLICANT: Gilbertson, Debra G.

TITLE OF INVENTION: SECRETED PROTEINS ENCODED BY HUMAN

TITLE OF INVENTION: CHROMOSOME 13

FILE REFERENCE: 97-38C1

CURRENT APPLICATION NUMBER: US/10/010,050A

CURRENT FILING DATE: 2002-03-26

PRIOR APPLICATION NUMBER: US 09/122,383

PRIOR FILING DATE: 1998-07-24

PRIOR APPLICATION NUMBER: US 60/053,613

PRIOR FILING DATE: 1997-07-24
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Sequence 26, Application US/10653595
Publication No. US20040048304A1
GENERAL INFORMATION:
APPLICANT: Ruben et. al.
TITLE OF INVENTION: 95 Human secreted proteins
FILE REFERENCE: PZ027P1C1
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LOCATION: (47)...(1084)
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PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/080,314
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080,312
PRIOR FILING DATE: 1998-04-01
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/078,578
PRIOR FILING DATE: 1998-03-19
PRIOR FILING DATE: 1998-03-19
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PRIOR FILING DATE: 1999-03-18
PRIOR APPLICATION NUMBER: 60/078,566
PRIOR FILING DATE: 1998-03-19
PRIOR PRIOR APPLICATION NUMBER: 60/078,576
PRIOR FILING DATE: 1998-03-19
PRIOR FILING DATE: 1998-03-19
PRIOR PRIOR DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/078,573
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/078,574
PRIOR FILING DATE: 1998-03-19
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SEQ ID NO 26
LENGTH: 1751
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CURRENT FILING DATE: 2003-09-03
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NAME/KEY: SITE
LOCATION: (1520)
OTHER INFORMATION: n equals a,t,g, or
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NAME/KEY: SITE
LOCATION: (1741)
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OTHER INFORMATION:
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LOCATION: (1735)
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OTHER INFORMATION:
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OTHER INFORMATION:
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ORGANISM: Homo sapiens
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US-09-397-945-26
; Sequence 26, Application US/09397945
; Publication No. US20030065139A1
US-10-010-050A-2_COPY_1_30 (1-30) x US-09-397-945-26
                                                             Query Match:
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PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/078,576
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/078,573
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/078,573
PRIOR APPLICATION NUMBER: 60/078,573
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CURRENT FILING DATE: 1999-09-17
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PRIOR APPLICATION NUMBER: 60/078,577
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/078,563
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PRIOR APPLICATION NUMBER: 60/080,314
PRIOR FILING DATE: 1998-04-01
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PRIOR APPLICATION NUMBER: 60/078,566
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TYPE: DNA
ORGANISM: Homo sapiens
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OTHER INFORMATION: n equals a,t,g,
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LOCATION: (152)
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LOCATION: (1741)
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; LOCATION: (1)...(1038)
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 13
                                                                                                                                                                       Sequence 13, Application US/10010050A
Publication No. US20020173624A1
GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
APPLICANT: Gilbertson, Debra G.
APPLICANT: GILDERTSON, Debra G.
TITLE OF INVENTION: CCHROMOSOME 13
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TITLE OF INVENTION: SECRETED PROTEINS ENCODED
TITLE OF INVENTION: CHROMOSOME 13
FILE REFERENCE: 97-38
FILE REFERENCE: 97-38
CURRENT APPLICATION NUMBER: US/09/122,383A
CURRENT FILING DATE: 1988-07-24
EARLIER APPLICATION NUMBER: 60/053,613
EARLIER FILING DATE: 1997-07-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Sheppard, Paul O. APPLICANT: Gilbertson, Debra
                                                                           CURRENT APPLICATION NUMBER: US/10/010,050A
CURRENT FILING DATE: 2002-03-26
CURRENT FILING DATE: US 09/122,383
PRIOR FILING DATE: 1998-07-24
PRIOR FILING DATE: 1998-07-24
SOFTWARE: FastSEQ for Windows Version
                    NUMBER OF SEQ ID NOS: 19
                                   PRIOR FILING DATE: 1997-07-24
                                                                                                                                                               FILE REFERENCE: 97-38C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Degenerate nucleotide sequence encoding zsig46 OTHER INFORMATION: polypeptide of SEQ ID NO:2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
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Matches:
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SEQ ID NO 13

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US-10-010-050A-2_COPY_1_30 (1-30) x US-10-027-632-241716 (1-580)
                                                                    Best Local Similarity:
Query Match:
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US-10-027-632-241716
                                                                                                     Percent Similarity:
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                  PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: 108827 129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
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                                                                                                                                                                                                                                  LENGTH: 580
TYPE: DNA
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LOCATION: (1)...(1038)
OTHER INFORMATION: n = A,T,C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 1999-09-28
                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 2000-02-24
APPLICATION NUMBER: US 60/167,363
                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 60/185,218
                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 60/146,002
                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 60/156,358
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Indels:
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Percent Similarity:
Best Local Similarity:
Query Match:
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PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILLING DATE: 2000-07-12
PRIOR FILLING DATE: 2000-04-20
PRIOR FILLING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILLING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/185,218
                                                                                                                                                                    Sequence 15190, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
                                            APPLICANT:
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                                                                            APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
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  APPLICANT:
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
FILE REFERENCE: 108827.129
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CURRENT FILING DATE: 2002-04-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/156,358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
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             Ohlsen, Kari
Zyskind, Judith
Wall, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                 GGTCATGCCAGTGCAAGAAGTGGGTTTCCATGG
Trawick, John
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Matches:
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Indels:
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PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2000-10-27
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR APPLICATION NUMBER: 60/269,308
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lest Local Similarity:
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SEQ ID NO 12900
LENGTH: 256
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APPLICANT: Warren, Wesley C.
                                                                                                                                                                                                                                                                                                                                                                                            Sequence 12900, Application US/09960352
Patent No. US20020137139A1
                                                   APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT FILLING DATE: 2001-09-24
CURRENT FILLING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
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PRIOR TILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECU
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
                                                                                                                                                                                             US-09-960-352-11275/c
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Best Local Similarity:
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                                                                                                                                Sequence 11275, Application US/09960352
Patent No. US20020137139A1
GENERAL INFORMATION:
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APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
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OTHER INFORMATION: Clone ID: 55-LIB3058-030-Q1-K1-F4
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; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 48-LIB34-036-Q1-E1-D8
US-09-960-352-11275
                                    RESULT 14
US-09-814-353-21894/c
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Best Local Similarity:
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CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 11275
LENGTH: 404
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Sequence 21894, Application US/09814353
Publication No. US20030165831A1
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APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION.
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
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ORGANISM: Bos taurus
OTHER INFORMATION: C.
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US-10-395-740-15
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CURRENT APPLICATION NUMBER: US/09/814,353
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: US 60/191,031
PRIOR FILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-05-25
PRIOR FILING DATE: 2000-05-25
PRIOR PILING DATE: 2000-06-15
PRIOR PILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: US 60/216,820
PRIOR APPLICATION NUMBER: US 60/216,820
PRIOR APPLICATION NUMBER: US 60/220,661
PRIOR APPLICATION NUMBER: US 60/220,661
PRIOR APPLICATION NUMBER: US 60/257,672
PRIOR PILING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 22037
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                                                                                                                                                                                                                                                                                                                                          Sequence 15, Application US/10395740 Publication No. US20030215852A1
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APPLICANT: Wood, Andrew
APPLICANT: Gulukota, Kamalakar
TITLE OF INVENTION: NOVEL PANCORTIN-PABLO PROTEIN INTERACTIONS AND METHODS
TITLE OF INVENTION: THEREOF
TILE REFERENCE: AM10375PCT
CURRENT APPLICATION NUMBER: US/10/395,740
CURRENT FILING DATE: 2003-03-24
PRIOR APPLICATION NUMBER: US 60/369,244
PRIOR PILING DATE: 2002-04-01
PRIOR PILING DATE: 2002-04-01
PRIOR PILING DATE: 2002-06-06
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APPLICANT: Lillie, James
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
                                                                                                                                                                                                                                                                        APPLICANT: WYETH APPLICANT: Mark
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LOCATION: 1, 2, 3, 4, 4827, 4828, 4829,
LOCATION: 4835, 4836, 4837, 4838, 4839,
LOCATION: 4845, 4846, 4847, 4848, 4849,
OTHER INFORMATION: n = A,T,C or G
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4841, 4842,
4851, 4852,
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NUMBER OF SEQ ID NOS: 15

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SOFTWARE: PatentIn version 3.2

SEQ ID NO 15
LENGTH: 44442
TYPE: DNA
DRANISM: Genomic DNA
IS-10-395-740-15

Alignment Scores:
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Score:
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US-10-010-050A-2_COPY_1_30 (1-30) Best Local Similarity: ; ORGANISM: Pseudomonas aeruginosa US-09-252-991A-9484 NUMBER OF SEQ ID NOS: SEQ ID NO 9484 LENGTH: 438 Sequence 9484, Application US/09252991A Patent No. 6551795 GENERAL INFORMATION: APPLICANT: Marc J. Rubenfield et al. TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: 107196.136 CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18 PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR APPLICATION NUMBER: US 60/074,798 PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27 PRIOR FILING DATE: 1998-07-27 ArgArgGlyAlaGlyAlaAlaArgGlyArgAlaSerTrp----CGGCGACCCGCTGCGGCGCTCGCAGGCGGCGGCGATGGCGGTGATCGACAGCGACGAGG 33.2 64.00 45.24% 40.48% 37.87% 33142 × US-09-252-991A-9484 (1-438) Length: Matches: Conservative: Mismatches: Indels: 438 17 9 14 64 14

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APPLICANT: MARC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING '
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 9378
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
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GENERAL INFORMATION:
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NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                               Rubenfield et al.

NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
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TITLE OF INVENTION: MUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
PILE REFERENCE: 107196.136
CURRENT FAPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
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PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
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Sequence 9347, Application US/09252991A Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.

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ercent Similarity:
est Local Similarity:
nery Match:
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IS-09-252-991A-13835/c
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S-09-252-991A-9347
                                                                           JS-10-010-050A-2_COPY_1_30 (1-30) x US-09-252-991A-13835 (1-2316)
                                                                                                                                                               Percent Similarity:
Best Local Similarity:
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SEQ ID NO 9347
LENGTH: 2274
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LENGTH: 2316
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                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18 PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR FILING DATE: 1998-02-18 PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27 NUMBER OF SEQ ID NOS: 33142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSETDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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Query Match:
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GENERAL INFORMATION:
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                                                                                                                                                                                 ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Zhang, Ke
APPLICANT: Max, Edward E
APPLICANT: Saxon, Andrew
TITLE OF INVENTION: 19E ISOFORMS AND METHODS OF USE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/037,57; FILING DATE: 24-MAR-1993
ATTORNEY/AGENT INFORMATION: NAME: Rowland, Bertram I
                                                                                                                                                                                                                                                                                                              STREET:
                                                                                                                                                                                                                                                                        STATE:
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                                       CLASSIFICATION:
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VVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS 
VVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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                                                                                                                                                                                                                                                       USA
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Embarcadero Center, Suite 3400
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US-08-601-184-4/c
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Patent No. 6043345
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REFERENCE/DOCKET NUMBER: A-57950/BIR UCIA-233
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299 FHT UR
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION: APPLICANT: Zhang,
                                                                                                                                                                                                                                                                                                                       APPLICANT: Saxon, Andrew
TITLE OF INVENTION: 1GE ISOFORMS AND METHODS OF USE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
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                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PCDOS/MSDOS SOFTWARE: PATENTIN Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                         ATTORNEY/AGENT INFORMATION
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TYPE: nucleic acid
                                                             FILING DATE: CLASSIFICATION: 530
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                                                                                                                                                                                                                                                                        CITY: San Francisco
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          NAME: Sherwood, Pamela J. REGISTRATION NUMBER: 36,677
                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                   ZIP: 941114187
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REFERENCE/DOCKET NUMBER: A-57950-1/PJS UCLA233-1
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89..172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDNA
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63.00
42.86%
36.73%
37.28%
                                                                                                 US/08/601,184
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Indels:
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                                                                                                                                    Version #1.25
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US-08-713-928B-8/c
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (415) 494-8701
TELEPAX: (415) 494-8771
TELEX: 910 277299 FHT UR
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
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APPLICANT:
APPLICANT:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/713,928B FILING DATE: 13-SEP-1996
                                                                                                                                                                                                                                                                                          APPLICANT: WEISSENBORN, DEBORAH L.
TITLE OF INVENTION: PRODUCTION OF LYSOSOMAL ENZYMES IN
TITLE OF INVENTION: PLANT-BASED EXPRESSION SYSTEMS
NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                   COUNTRY: USA
                                                                                                                                                                                                                    STATE: New York
                                                                                                                                                                                                                                                  STREET:
                                                                                                                                                                                                                                                                 ADDRESSEE:
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                                                                                                                                                                                                                                     New York
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                                                                                                                                                                                                                                                   1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                      CRAMER, CAROLE OISHI, KAREN K.
                                                                                                                                                                                                                                                                                                                                                                  RADIN, DAVID N.
CRAMER, CAROLE L.
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89..172
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63.00
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Matches:
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4 20
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IS-10-010-050A-2_COPY_1_30 (1-30) x US-08-713-928B-8 (1-2067)
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S-09-191-171-4/c
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West Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No. 6149909
Patent No. 6149909 6143294
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/09191171
           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
PILING DATE: 23-UTN-1995
APPLICATION UNMBER: AU PK9
FILING DATE: 14-NOV-1991
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (212) 869-974
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
APPLICANT:
                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/191,171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
COLLY SCOTT MURPHY & PRESSER STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7956-0011-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741
TELEX: 66141 DENNYTY
                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: HOPWOOD, John J.

TITLE OF INVENTION: SYNTHETIC ALPHA-L-IDURONIDASE AND GENETIC TITLE OF INVENTION: SEQUENCES ENCODING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
APPLICATION NUMBER:
                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Coruzzi, Laura A. REGISTRATION NUMBER: 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1021 AGGCGGAGGTGGTGTTGGCCAGTAGCA 995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORSBORN, Annette M.
NELSON, Paul V.
CLEMENTS, Peter R.
MORRIS, Charles P.
                                                                                                                                                                                                                                                                                                                     USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANSON,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SCOTT, Hamish S. ANSON, Donald S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     unknown
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62.50
48.28*
44.83*
36.98*
                                                    AU PK9490/91
                                                                                      US 08/494,104
AU PCT/AU92/00611
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Indels:
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Matches:
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Best Local Similarity:
Query Match:
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4, Application US/09385707 Patent No. 6238662
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: ISM PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/385,707
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: SCOTT, Hamish S.
APPLICANT: ANSON Donald S.
APPLICANT: ORSBORN, Annette M.
APPLICANT: NELSON, Paul V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 516-742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO:
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ETILING DATE: 07-UUL-1993
ATTORNEY_AGENT INFORMATION:
NAME: DIGIGIO, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 8978
TELECOMMUNICATION INFORMATION:
TELEPHONE: 516-742-4343
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                      APPLICANT: CHMENTS, Peter R.
APPLICANT: MORRIS, Charles P.
APPLICANT: HOPWOOD, John J.
TITLE OF INVENTION: SYNTHETIC ALPHA-L-IDURONIDASE AND GENETIC TITLE OF INVENTION: SQUENCES ENCODING SAME NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: CDNA
                                                                                                                                                                               STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
                                                                                                                                                  COUNTRY: U
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TELEPHONE: 516-742-4366
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TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY:
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89..2047
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Matches:
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                                                  Version
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/4
FILING DATE:
ATTORNEY/AGENT INFORMATION:

08/494,104

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Percent Similarity:
Best Local Similarity:
Query Match:
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LOCATION:
US-09-385-707-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 13
US-09-639-696C-4/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4, Application US/09639696C Patent No. 6524835
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 516-742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 2155 base pairs
TYPE: nucleic acid
STRANDEDWESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: 516-742-4343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/639,696C
FILING DATE: 16-Aug-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: DiGiglio, Frank S. REGISTRATION NUMBER: 31, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                ORSBORN, Annette M.

NELSON, Paul V.

CLEMENTS, Peter R.

MORRIS, Charles P.

HOPWOOD, John J.

TITLE OF INVENTION: SYNTHETIC ALPHA-L-IDURONIDASE AND GENETIC SEQUENCES ENCODING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1169 CGAAGGGGTGCGGGTAGCTCAGGAAGGCATTGTCGTTGCTCAGGAGCGCGTAGGGA
                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON PEABODY LLP
                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: SCOTT,
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                                                                                                                                                                                                      STREET: 990 Stewart Avenue
CITY: Garden City
STATE: New York
COUNTRY: USA
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48.28%
44.83%
36.98%
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Donald S.
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Indels:
Gaps:
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US-09-191-171-7/c
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                             Sequence 7, Application US/09191171
Patent No. 6149909
Patent No. 6149909 6143294
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APPLICANT: SCOTT, Hamish S.
APPLICANT: ANSON, Donald S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 2155 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                APPLICANT:
APPLICANT:
                                                                                                                                                                                    APPLICANT: CLEMENTS, Peter R.
APPLICANT: MORRIS, Charles P.
APPLICANT: HOPMOOD, JOHN J.
TITLE OF INVENTION: SYNTHETIC ALPHA-L-IDURONIDASE AND GENETIC
TITLE OF INVENTION: SEQUENCES ENCODING SAME
                  COMPUTER READABLE FORM:
                                                                                                                                                NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
MEDIUM TYPE: Floppy disk
                                  COUNTRY: U
                                                                                                          STREET:
                                                                                                                                ADDRESSEE:
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NAME: Pokalsky, Ann R.
REGISTRATION NUMBER: 34,697
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 516-832-7572
TELEFAX: 516-832-7555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1169 CGAAGGGGTGCGGGTAGCTCAGGAAGGCATTGTCGTTGCTCAGGAGCGCGTAGGGA 1110
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                                                                      r: 400 Garden City Plaza
  Garden City
: New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 08/084,254 FILING DATE: 07-JUL-1993
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APPLICATION NUMBER: AU PK9490/91
FILING DATE: 14-NOV-1991
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LOCATION: 89..2047
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                                                        USA
                                                                                                                                                                                                                                                                                ORSBORN, Annette
                                                                                                                                SCULLY SCOTT MURPHY & PRESSER
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36.98%
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Indels:
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SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:

PC-DOS/MS-DOS

APPLICATION NUMBER: US/09/191,171

FILING DATE:

COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS

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'S-10-010-050A-2_COPY_1_30 (1-30) x US-09-191-171-7 (1-4480)
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est Local Similarity:
APPLICANT: ORSBORN, Annette M.
APPLICANT: NELSON, Peter R.
APPLICANT: CLEMENTS, Peter R.
APPLICANT: MORRIS, Charles P.
APPLICANT: MORRIS, Charles P.
APPLICANT: MORRIS, CHARLES P.
APPLICANT: MOPWOOD, John J.
TITLE OF INVENTION: SYNTHETIC ALPHA-L-IDURONIDASE AND GENETIC TITLE OF INVENTION: SEQUENCES ENCODING SAME
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSE: SCULLY SCOTT MURPHY & PRESSER
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                 1S-09-385-707-7/c
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Patent No. 6238662
GENERAL INFORMATION:
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LENGTH: 4480 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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ATTORNEY AGENT INFORMATION:
NAME: DIGIGIO, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE, DOCKET NUMBER: 8978
TELECOMMUNICATION INFORMATION:
TELEPHONE: 516-742-4343
TELEPAX: 516-742-4366
                                                                                                                                                                                                                                           APPLICANT:
APPLICANT:
APPLICANT:
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FILING DATE: 12-NOV-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: AU PK9490/91 FILING DATE: 14-NOV-1991 PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 08
FILING DATE: 23-JUN-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 08/084,254
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                                                                                                                                                                                                                                                                                     SCOTT, Hamish S. ANSON, Donald S.
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62.50
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Matches:
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Search completed: April 25, 2004, 05:51:41 Job time : 12.9583 secs
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                 Score:
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TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 4480 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
ATTORY/AGENT INFORMATION:
NAME: Didigilio, Frank S.
NAME: Didigilio, Frank S.
REGISTRATION NUMBER: 31,346
REFRENCE/DOCKET NUMBER: 8978
TELECOMMUNICATION INFORMATION:
TELEPHONE: 516-742-4343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: (
                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                2192 CGAAGGGGTGCGGGTGGTAGCTCAGGAAGGCATTGTCGTTGCTCAGGAGCGCGTAGGGGA 2133
                                                                        2132 AGGCGGAGGTGTTGGCCAGTAGCA 2106
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                                                                                                      ArgAlaSerTrpCysTrpAlaLeuAla 19
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62.50
48.28*
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Matches:
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Indels:
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13
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MODEL=frame+_p2n.model -DEV=xlh
Q=/cgn2 1/USPT0 spool/US10010050/runat_22042004_113203_27539/app_query.fasta_1.1372
DB=N_Geneseq_29Jan04 -OpMT=fastap_-SUFFIX=rng_-NINMATCH=0.1 -LOOFCL=0
LOOFEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
MODE=LOCAL -OUTFMT=pto -NORM-ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
USER=US10010050 @GGN 1 1819 @runat 22042004 113203_27539 -NCPU=6 -ICPU=3
NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
NORM-CARRON TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
PGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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No.
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Maximum Match 100%
Listing first 45 summaries
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Match
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Ygapop 10.0 , X
Ygapop 6.0 , I
Fgapop 6.0 , I
Delop 6.0 , I
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geneseqn2001as:*
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Aax02855 Human zsi
Aaz24826 Human sec
Aak94829 Human ful
Abq40653 Oligonucl
Abq40653 Oligonucl
Abq13702 Oligonucl
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AAQ76361	ADC30433	AAK74135	AAL37818	ABL29392	ABL29393	ADA71534	ACA42256	ACC57671	AAA58471	ACA43808	AAS80870	ABL04056	AAS67958	AAS67953	ABK12169	ABK84080	ADD08990	AAX53491	ABZ97130	AAF21436	ABZ96537	AAF20843	AAA34721	AAX55273	ABZ96032	AAF20338	AAA34216	AAX54769	ABX48930	ABX46110	ABX40924	ADC08897	ABX47735	ACA27320	AAX02866	ABQ13703	
Aaq76361 Human imm	0433 Human	Human	Wheat KC		Dros	Ada71534 Rice gene	Prokar			Pro)		Abl04056 Drosophil	Aas67958 DNA encod	Aas67953 DNA encod	Human	Aax55273 Human enz	Human	Human		769 Endoth	Boviné	10 Bovine	24 Bovin	Rice DN	7735	320 Proka	Aax02866 Human deg	703 Oligc									

ALIGNMENTS

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08-JUL-1999;
11-JAN-2000;
02-MAY-2000;
                                                                                                                                                                                                                                                                   Human; full length cDNA; cDNA synthesis; oligo-capping; ss
                                                                                                                   07-JUL-2000; 2000EP-00114089
                                                                                                                                                          05-SEP-2001.
                                                                                                                                                                                                 EP1130094-A2.
                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                              Human cDNA clone representative sequence,
                                                                                                                                                                                                                                                                                                                                                       06-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                   AAK93424 standard; cDNA; 697 BP
(HELI-) HELIX RES INST.
                                                       99JP-00194486.
2000JP-00118774.
                                       2000JP-00183765
                                                                                                                                                                                                                                                                                                                SEQ ID NO: 1884.
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830 Primers useful for synthesizing full length cDNA clones and their use

WPI; 2001-524255/58.

Ota T,

Nishikawa T, su A, Sugiyama

Isogai T, na T, Nagai

Hayashi K, K, Kojima

Ishii S, u S, Otsuki

Kawai T, K ۲, H

'n

genetic manipulation

Example 11;

SEQ ID NO 1884; 1380pp + Sequence Listing; English.

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RESULT 2
AAKS921S
XX AAKS9
XX AAKS9
XX AAKS9
XX Huma
XX Huma
XX Huma
XX Huma
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OS Hom
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                                                                                                                                                                                                                                                                                                                  08-JUL-1999;
11-JAN-2000;
02-MAY-2000;
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                                                                        830 Primers useful for synthesizing full length cDNA clones and their use
                                                                                                                                                                                                             Ota T,
                                                                                                                             WPI; 2001-524255/58
                                                                                                                                                                                       Wakamatsu
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                                                  genetic manipulation.
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                                                                                                                                                                                                             Nishikawa T,
                                                                                                                                                                                                                                                                  HELIX RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MetArgArgGlyAlaGlyAlaAlaArgGlyArgAlaSerTrpCysTrpAlaLeuAlaLeu
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                                                                                                                                                                                                                                                                                                                  99JP-00194486.
2000JP-00118774.
2000JP-00183765.
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ma T, Nagai
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K, Kojima
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1 S, Otsuki
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T, Koga
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Claim

2; SEQ ID NO 618; 1380pp

+ Sequence Listing; English

New secreted polypeptide, zsig46, and its fragments, related fusion

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AAX02855
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DB:
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5' - and 3' -ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is the nucleotide sequence of the 5'-end of a cDNA provided in the invention. Note: The sequence data for this pattent did not form part of the printed specification, but was obtained in CD-ROM format directly from EPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 697 BP; 183 A; 160
                                                                                                                                                                                                                                                                                                                                   Secreted protein; zsig46; human; chromosome 13; thyroid; disease; hypothyroidism; Graves' disease; thyrotoxicosis; thyroid cancer; Hirschsprung's disease; neuronal ceroid-lipofucinosis; Wilson disease; Reiger syndrome; immunoassay; detection; anti-idiotypic antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                   14-MAY-1999
                                                                                                                                                                                                                                                         CDS
                                                                                                                                                                                                                                                                                                                                                                                                       Human zsig46 DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAX02855;
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                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                          therapy; diagnostic; ss.
                         P-PSDB;
                                                              Sheppard PO,
                                                                                                                   24-JUL-1997;
                                                                                                                                              24-JUL-1998;
                                                                                                                                                                                                    WO9905275-A1
                                                                                        (ZYMO ) ZYMOGENETICS INC.
                                       1999-142930/12.
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lest Local Similarity:
    19-MAR-1998;
19-MAR-1998;
19-MAR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; ds; immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    cognitive disorder; schizophrenia, prostate; obesity; osteoclast; thymus; osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion; endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
                                                                                                                                                    18-MAR-1999
                                                                                                                                                                                                                                23-SEP-1999
                                                                                                                                                                                                                                                                                                            WO9947540-A1
                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 27; Page 88-90; 101pp; English.
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    used for diagnosis and treatment of thyroid disorders
involving genes on chromosome 13.

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98US-0078566P.
98US-0078573P.
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19-MAR-1998;
19-MAR-1998;
19-MAR-1998;
19-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence represents a nucleic acid molecule which encodes a secreted human protein. The gene number, and the clone it is derived from, are detailed in the descriptor line. The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin Fc portion (e.g. AAZ24802) for increasing the stability of the fused protein as compared to the human protein only. The invention relates to 95 novel genes and their fragments (nucleic acid sequences: AAZ24811-Z24907; amino acid sequences AAY41308-Y41404) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the amount of the new polypuscleotides. Specific uses are described for each of the 95 polynucleotides, based on which tissues they are most highly expressed in (see AAZ24811 for described uses)
                        Human; full length cDNA; cDNA synthesis; oligo-capping;
                                                  Human
                                                                             06-NOV-2001
                                                                                                       AAK94829;
                                                                                                                                  AAK94829 standard;
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01-APR-1998;
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                                                 full-length cDNA,
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98US-0080314P.
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                                                  SEQ ID NO: 3977.
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Percent Similarity:
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RESULT 5 / C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-JUL-1999;
11-JAN-2000;
02-MAY-2000;
                          drug; side effect; cancer; central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphism; SNP; cell differentiation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2120
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                                                                    Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
                                                                                                      Oligonucleotide for detecting cytosine methylation SEQ ID NO 27244.
                                                                                                                                    12-JUL-2002
                                                                                                                                                                                              ABQ40653 standard; DNA; 630 BP
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genetic manipulation.
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DB; AAM93870.
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2000JP-00118774.
2000JP-00183765.
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a T, Nagai K, Kojima
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Otsuki T, Koga
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Determining the degree of cytosine methylation in genomic DNA, diagnosis and prognosis, comprises selective hybridization of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-371829/40
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05-SEP-2000;
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               Oligonucleotide for detecting cytosine methylation SEQ ID NO 27243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 630 BP; 219 A; 255
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                                                12-JUL-2002
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2000DE-01044543
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This invention describes a novel method for determining the degree of C methylation of a particular cytosine in a motif 5'-CpG-3', present in a C genomic sample of DNA. The sample is treated chemically to convert C cytosine (C) but not methylated C, to uracil, then part of the genomic C DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one member, C of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the C degree of hybridisation to both classes is determined from the label on C the amplicon. From the ratio of labels hybridised to the two classes of coligoners, the degree of methylation is calculated. The method is used: (i) for diagnosis and/or prognosis of side effects of therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders of the central C nervous, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide polymorphisms (SNP's); and (ii) for differentiation of cell or tissue types and for investigating cell differentiation. The method allows the methylation c status of many C residues to be determined simultaneously. ABQ13410-C ABQ54121 regreenty genomic DNA sequences used to illustrate the method constitution of disclosure of the invention
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05-SEP-2000; 2000DE-01044543.
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x ABQ13702 (1-631)

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This invention describes a novel method for determining the degree of cc methylation of a particular cytosine in a motif 5'.CpG-3', present in a cc genomic sample of DNA. The sample is treated chemically to convert cytosine (C) but not methylated C, to uracil, then part of the genomic CDNA that contains the target C is amplified to form a labeled amplicon. CC The amplicon is hybridised to two classes, each with at least one member, co degree of hybridisation to both classes is determined from the label on the amplicon. From the ratio of labels hybridised to the two classes of CC oligomers, the degree of methylation is calculated. The method is used: CC in for diagnosis and/or prognosis of side effects of therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders of the central conservous, cardiovascular, gastrointestinal and respiratory systems etc., CC particularly by detecting mutations or single nucleotide polymorphisms (SNP's); and (ii) for differentiation. The method allows the methylation convestigating cell differentiation. The method allows the methylation status of many C residues to be determined simultaneously. ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the method conference of the invention o
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gastrointestinal; respiratory system; single nucleotide polymorphism;
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                                                                                                                                                            cc rhis invention describes the isolation of a novel human secreted protein, cz zsig46 encoded by a gene on chromosome 13 which is mainly expressed in ct the thyroid. This product can be used to study secretion of proteins from cc cells and also to treat or prevent deficient expression of zsig46, which cc may be associated with thyroid diseases (e.g. hypothyroidism, Graves' cd disease, thyrotoxicosis, thyroid cancer etc.) or with diseases that involve genes in the same region of chromosome 13 (e.g. Hirschaprung's cc disease, neuronal ceroid-lipofucinosis, Wilson disease and Reiger syndrome). Antibodies and other binding proteins, are used as immunoassay creagents to detect zsig46 or cells expressing it, e.g. for assessing thyroid function to produce anti-idiotypic antibodies, for affinity purification of zsig46, to screen expression libraries, to neutralise zsig46 activity, and to deliver toxins, radioisotopes etc. for therapeutic or diagnostic purposes. Agoniets of the product can be used to promote growth, differentiation and proliferation of specific cell types, e.g. for treating (extra)thyroid diseases or as additive to cell
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                                                                                                                     Sequence 1038
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 diseases involving genes on chromosome 13.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             therapy; diagnostic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Reiger syndrome; immunoassay; detection; anti-idiotypic antibody;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Page 94-95; 101pp; English.
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MetArgArgGlyAlaGlyAlaAlaArgGlyArgAlaSerTrpCysTrpAlaLeuAlaLeu ATCMGNMGNGGNGCNGCNGCNMGNGGNMGNGCNWSNTGGTGYTGGGCNYTNGCNYTN 60

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CA27320
       C polypeptide of its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular to proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound a activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wang
Wall
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06-SEP-2001; 2001US-0094893.
25-0CT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
                                                                                                                                                                                                                                                              the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated nucleic acid; (2) a host cell containing the vector; (3) an isolated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-MAR-2002; 2002WO-US009107.
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                                                                                                                                                                                                                                                                                                                                                                                                          Claim 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            isolate candidate molecules for rational drug discovery programs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ELIT-)
                                                                                                                                                                                                                                                                                                                                                   invention relates to an isolated nucleic acid comprising any one 6213 antisense sequences given in the specification where express
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DB; ABU23450.
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Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 15190; 1766pp; English.
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Yamamoto R,
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Foreyth
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                        New nucleic acid associated with lactation, and muscle and deposition, useful for genome mapping, gene identification cattle breeding, or for genetically improving cattle.
                                                                                                                                                                                                                                                                                                                                                                   Bovine; ss; EST; expressed sequence tag; lactation; muscle deposition; fat deposition; genome mapping;
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(TAON/)
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11-JAN-2000;
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                                                                                                                                                                                                                                                                                                          US2002137139-A1
                                                                                                                                                                                                                                                                                                                                                         gene analysis; cattle breeding.
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                                                                                                                                                           WARREN W C.
                                                                                                                                                                                  MATHIALAGAN N.
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                                                                                                                                                                                                                                                                                                                                                                      genome mapping; gene
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cene identification;
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lactation or muscle and

The invention relates to a purified nucleic acid molecule

deposition

(designated

LMFD),

derived associated with Claim 2; SEQ ID NO 12900; 245pp; English

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RRESULT 1:
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                                  22-JUN-2001; 2001US-0300112P.
26-SEP-2001; 2001US-0325277P.
20-DEC-2001; 2001US-0342327P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               plant biotechnology; carbohydrate synthesis; carbohydrate metabolism; carbohydrate degradation; carbohydrate; plant grain; grain filling; corr.; tomato; banana; canola; cotton; peanut; sorghum; tobacco; sugarbeet; wheat; rice; protein; oil; starch; fibre; moisture content; cereal grain.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rice DNA sequence Seq ID323 related to grain filling.
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RESULT 14
ABX40924/c
ID ABX409
XX ABX409
XX ABX409
XX BOVINE
XX BOVINE
XX BOVINE
XX Gene a
XX Gene a
XX US2002
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XR 12-JAN
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       polymuclectides comprising a nuclectide sequence encoding a protein which is involved in or associated with the synthesis, metabolism or degradation of carbohydrates in the plant grain and the expression of which is up-regulated during grain filling. The plant is selected from corn, tomato, banana, canola, cotton, peanut, sorghum, tobacco, sugarbeet, wheat, and rice. The invention may be useful for the improvement of protein, oil, starch, fibre and moisture content of the cereal grains. In addition, carbohydrate levels may be modified to a more desirable level using the present invention. The present sequence is a DNA sequence encoding a rice protein of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New plant genes encoding polypeptides having an activity involved in or associated with the synthesis, metabolism or degradation of carbohydrates in the plant grain useful in generating plants having improved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zhu T, Cheng W, Briggs S, Glazebrook J, Katagiri F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This invention, in the area of plant biotechnology, relates to novel
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                                                                                                 US2002137139-A1
                                                                                                                                                                           Bovine; ss; EST; expressed sequence tag; lactation; IMFD; muscle deposition; fat deposition; genome mapping; gene i
                                                                                                                                                                                                                               Bovine EST associated with lactation/muscle/fat deposition #6089
                                                                                                                                                                                                                                                                                                  ABX40924;
                                                                                                                                                                                                                                                                                                                                   ABX40924 standard; cDNA; 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ftp.wipo.int/pub/publishedpct_sequences.
                                24-SEP-2001; 2001US-00960352
                                                                 26-SEP-2002
                                                                                                                                Bos Taurus
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)B; ADC08057.
                                                                                                                                                              analysis; cattle breeding.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CGCCGGGGTTCAGGTTCCACCCGAGGGACGACGAGCTGGTGCTGGACTACCTCCTGCACA 94
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Kreps J, Provart N,
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Ricke D;
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12-JAN-1999;

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Clactation or muscle and fat deposition (designated LMPD), derived from C cattle, and the LMFD nucleic acid can specifically hybridise to a second C nucleic acid molecule comprising any of 15112 nucleotide sequences, C appearing as ABX34836-ABX49947, or complements of them. Also included are (1) a transformed cell having a nucleic acid comprising an LMFD nucleic acid linked to a promoter and a 3 non-translated sequence that C functions in the cell to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and C (2) determining a level or pattern of a molecule in a bovine cell or tissue comprising: (a) incubating a marker nucleic acid comprising any of the 15112 nucleic acid sequences or its complement or fragment) with a complementary nucleic acid molecule obtained from the bovine cell or tissue, where hybridisation between the marker nucleic acid and the complementary nucleic acid permits the detection of the molecule; and (b) detecting the level or pattern of the complementary nucleic acid is predictive of the complementary nucleic acid is nad nalysis, cattle breeding, preparation of constructs for use in cattle gene expression, cr for genetically improving cattle. The present sequence is one of the present sequence was not shown in the specification but was obtained in electronic format from the USPTO web site:
RESULT 15
ABX46110/c
ID ABX461
KX
AC ABX461
KX
TO ABX461
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puery Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a purified nucleic acid molecule associated with lactation or muscle and fat deposition (designated LMFD), derived from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-110599/10
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    Bovine EST
                                                                                           ABX46110
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                                             21-FEB-2003
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                                                                                                                                                                                                                                                                                                                          GGAGCAGGTGCATCACGTGGTCCTGTGTCATGCTGCCGTACTTGGTGGCGTTCTTCATGG
                                                                                                                                                                                                                                                                                                                                                                 GlyAlaGlyAlaAlaArgGlyArgAlaSerTrpCys----
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    associated with lactation/muscle/fat deposition #11275
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41.12%
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(BYAT/)
(MATH/)
(TAON/)
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11-JAN-2000;
                                                                                                                                                                                                                  24-SEP-2001; 2001US-00960352
                                                                                                                                                                                                                           26-SEP-2002.
                                                                                                                                                                                                                                    US2002137139-A1
                                                                                                                                                                                                                                                     gene analysis; cattle breeding.
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                                                                                                                                                                              WARREN W C.
                                                                                                                                                                                           BYATT
                                                                                                                                                                                       MATHIALAGAN
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2000US-00480902
                                                                                                                                                                                           J С.
                                                                                                                                                                     z
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                                                                                                                                                                      Warren WC
                                                                                                                                                                                                                                                           identification;
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New nucleic acid associated with lactation, and muscle and deposition, useful for genome mapping, gene identification cattle breeding, or for genetically improving cattle. analysis

WPI; 2003-110599/10

Claim 2; SEQ ID NO 11275; 245pp; English.

Clactation or muscle and fat deposition (designated implementary muscle and fat deposition (designated impl), derived from cattle, and the IMFD nucleic acid can specifically hybridise to a second coursels acid molecule comprising any of 15112 nucleotide sequences, complements of them. Also included are coid linked to a promoter and a 3′ non-translated sequence that coid linked to a promoter and a 3′ non-translated sequence that coid polyadenylated ribonucleotides to a 3′ end of the mRNA molecule; and complementary nucleic acid sequences or its complementary nucleic acid sequences or its complement or fragment) with a complementary nucleic acid molecule or its sue, where hybridisation between the marker nucleic acid and the complementary nucleic acid molecule obtained from the bovine cell or the detection of the complementary nucleic acid molecule obtained from the molecule; and (b) detecting the level or pattern of the complementary nucleic acid, where complementary nucleic acid molecule. The IMFD nucleic acid is used for the detection of the molecule. The IMFD nucleic acid is used for cording, preparation of the molecule. The IMFD nucleic acid is used for the setting, preparation of constructs for use in cattle gene expression, or for genetically improving cattle. The present sequence is one of the present sequence was not shown in the sequence tag) nucleic acids. Note: The corsents sequence was not shown in the sequence tag) nucleic acid and in a cordinal process of the corporation of the molecule in a bovine cell or tissue. The invention relates to a purified nucleic acid molecule associated with lactation or muscle and fat deposition (designated LMFD), derived from seqdata.uspto.gov/sequence.html?DocID=20020137139 electronic present sequence was not shown in the specification format from the USPTO web site:

US-10-010-050A-2_COPY_1_30 (1-30) Query Match: Best Local Alignment Scores: Percent Similarity: Similarity: 31.4 69.50 48.48% 45.45% 41.12% x ABX46110 Matches: Conservative: Mismatches: Indels:

Sequence 404

BP;

91 A; 131

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115

G; 67

Ή, 0 ů

Ş 덩 304 GGAGCAGGTGCATCACGTGGTCCTGTGTCATGTTGCCGTACTTGGTGGCGTTCTTCATGG 4 GlyalaGlyalaAlaArgGlyArgAlaSerTrpCys---ĞŢ

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

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Domaind line parameters:
MODEL=frame+ p2n.model -DEV=Xlh
MODEL=frame+ p2n.model -DEV=Xlh
Q=/cgn2_1/USPTO_spool/US10010050/runat_22042004_113204_27556/app_query.fasta_1.1372
DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
.UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
.UNITS=bits -START=1 -END=-1 -MATRIX=15-losum62 -TRANS=human40.cdi -LIST=45
.DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODELCCAL
.OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
.USER=US10010050 @CGN 1 1 6283 @xunat 22042004 113204 27556 -NCPU=6 -ICPU=3
.NO MMAP -LARGEQUERY -NEG SCORES 0 -WAIT -DSPBLOCK=100 -LONGIOG
.DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
.PEV TIMEOUT=120 -WARN TIMEOUT=30.5 -DELDOP=6 -DELEXT=7
.FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELDOP=6 -DELEXT=7
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Maximum Match 100%
Listing first 45 summaries
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seq length: 2000000000
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154
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
          27513289 seqs, 14931090276 residues
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29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

REFERENCE	ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION		DEFINITION	LOCUS	AU280382	RESULT 1
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleoscomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 565)	Homo sapiens	Homo sapiens (human)	EST.	AU280382.1 GI:28299609	AUZ80382	RECIPICE.	AU280382 NIESE2 Homo sapiens cDNA clone NIESE2001763 5', mRNA	AU280382 565 bp mRNA linear EST 31-JUL-2003		

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Redifferentiation of dedifferentiated chordcocytes and chondrogenesis of human bone marrow stromal cells via chondrosphere formation with expression profiling by large-scale cDNA analysis exp. Cell Res. 288 (1), 35-50 (2003)
                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 607)

Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,X., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: genomics@hri.co.jp

HRI human cDNA Project, Sugiyama,T.; Wakamatsu,A.; Irie,R.;

Umezzawa,A.; Fukuma,M.; Kusakari,S.; Hata,J.; Ishii,S.; Yamamoto,

Isono,Y.; Saito,K.; Nakamura,Y.; Masuho,Y.; Nagai,K.; Isogai,T.

HRI human cDNA project; cDNA library construction & 5'-end one

pass sequencing: Helix Research Institute.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
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BM849262
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К-EST0129297 Sl3KMS5 Homo sapiens cDNA clone Sl3KMS5-67-D07 5',
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          52 Eoeun-dong Yuseong-gu, Tel: +82-42-860-4470
                                                                                                                                                                                                                                                                                                                           BM849262.1 GI:19205661
                                                 Korea Research Institute of Bioscience & Biotechnology
                                                                   Genome Research Center
                                                                                     Contact: Kim YS
                                                                                                          Unpublished (2002)
                                                                                                                            Kim, Y.S.
21C Frontier Korean EST Project 2001
                                                                                                                                                                                                                                                                   Homo sapiens
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Plate: 67 row: D column: 07
                                                                                          Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K., Lemishka,I., Scearce,M., Brestelli,J., Gradwohl,G., Clitton,S., Hillier,L., Marra,M., Pape,D., Wylle,T., Martin,J., Blistain,A., Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R., Williams,T., Jackson,Y. and Bowers,Y.
                                                                                                                                                                                                                                                                       Homo sapiens
                              Endocrine Pancreas Consortium Unpublished (2000) Other ESTs: ik38b05.x1
                                                                                                                                                                                                                                                                                                                                 BQ417448.1
Endocrine Pancreas Consortium
              Contact: Douglas Melton, Klaus H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LeuTrpLeuAlaValValProGly 28
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/lab host="Top10F'"
/clone lib="S13KMS5"
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/mol_type="mRNA"
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/notes—Tvector: PCNS; Site 1: EcoRI; Site 2: NotI; The poly (A) + RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoR I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oilgo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors
                                               strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F' by electroporation method. The cDNA libraries
constructed by this method are full-length enriched cDNA
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623 bp mRNA linear EST 15-JUL-2003 ik38b05.yl HR85 islet Homo sapiens cDNA clone IMAGE:5783001 5' similar to SW:CLN5_HUMAN 075503 CLNS PROTEIN. [1] ;, mRNA sequence. BQ417448 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Arecedecedecedecedecicedes Acedecirio de la compara de la MetArgArgGlyAlaGlyAlaAlaArgGlyArgAlaSerTrpCysTrpAlaLeuAlaLeu 20 Conservative: 000026 EST 15-JUL-2003

& Hiroshi Inoue

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RESULT 4
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Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: David N. Louis, M.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incytte Genomics, Inc.

Clone distribution: MGC clone distribution information can
                                                                                                                                                    NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
1 (bases 1 to 676)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Library was constructed by Dr. Hiroshi Inoue DNA sequencing by: Washington University Genome Sequencing Center For information obtaining a clone please contact: Dr. Hiroshi Inoue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: dmelton@biohp.harvard.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Harvard University, Howard Hughes Medical Institute Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
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602782325F1 NCI_CGAP_Brn67 Homo
                                                                                                                                                                                                                                                                                        Homo sapiens
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone libe "HR85 islet"
/clone libe "HR85 islet"
/note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1:
Not1; Site_2: Xho1; cDNA made by oligo-dT priming.
Size-selected on agarose gel. Average insert size -1kb. 5'
XhoI site was destroyed after directional cloning.
Amplified once. Contact information: Hiroshi Inoue, MD,
Metabolism Div. (Alan Permutt Lab), Washington University
School of Medicine, Box 8127, 660 South Euclid Ave., St.
Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
314-362-1916, Fax: 314-747-2692."
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/clome="IMAGE:5783001"
/tissue_type="purified pancreatic islet"
/lab_host="DH10B"
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   found through the I.M.A.G.E. Consortium/LLNL http://image.llnl.gov plate: LLAM10860 row: a column: 07
                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 787)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mRNA sequence.
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cDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information
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Location/Qualifiers
                                                                                                                                                          quality sequence stop: 762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /lab_host="DH10B (TI phage-resistant)"
/clone_lib="NCI_CGAP_Brn67"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2.3 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
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/db_xref="taxon:9606"
/clone="IMAGE:4933134"
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tissue_type="cervical carcinoma cell line"
/lab_host="DH10B"
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                                                             /mol_type="mRNA"
/db_xref="taxon:9606"
                                            clone="IMAGE:5105093"
                                                                                                 organism="Homo sapiens"
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cDNA clone IMAGE:5105093 5',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: cgapbs r@mail.nih.gov
Tissue Procurement: Dr. James R. Lupski
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13590 row: n column: 18
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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AGENCOURT 8103813 Lupski sympathetic_trunk Homo sapiens cDNA clone
IMAGE:619\overlightarrow 5', mRNA sequence.
BQ719074
BQ719074.1 GI:21857971
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/note="Organ: cervix; Vector: pCMV-SPORT6; Site 1: Not1;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.4 kb. Library prepared by Life
Technologies."
              /clone lib="Lupski sympathetic trunk"
/note="Vector: pCMV-SPORT6 (Life Technologies); Site_1:
Not1; Site_2: Sall; cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:
5'-TCGACCCACGCGTCCG-3' and
5'-GACTAGTTCTAGATCGCGAGCGGCCCT(15)-3'. Size selected >
1'kb for average insert length 1.9 kb. This is a primary
library, non-amplified. Library constructed by Life
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine); available through Life
Technologies
                                                                                                                                                                                                                                                    /tissue type="sympathetic trunk"
/dev_stage="adult, 16 yr"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                          organism="Homo sapiens"
/mol_type="mRNA"
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'clone="IMAGE:6191057"
                                                                                                                                                                                                                                                                                                                             sex="male"
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Best Local Similarity:
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                                Query Match:
DB:
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US-10-010-050A-2_COPY_1_28 (1-28) x BI090566 (1-869)
                                                               Percent Similarity:
Best Local Similarity:
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1 (bases 1 to 869)

NIH-MCC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                           Plate: LLAM11023 row: a column:
High quality sequence stop: 843.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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                                                                                                                                                                                                                                                                                                                                                                                                                           found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                        cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D
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                                                                                                                                                                          /clone lib="NIH_MGC 10"
/note="Organ: cervix; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.5 kb. Library prepared by Life
Technologies."
                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                             /clone="IMAGE:4996891"
/cell_line="MGC36"
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MetArgArgGlyAlaGlyAlaAlaArgGlyArgAlaSerTrpCysTrpAlaLeuAlaLeu 20

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Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization unpublished (2001)
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923 bp mRNA linear EST 01-MAY-200:
EX331615 Homo mapienm NEUROBLASTOMA COT 10-NORMALIZED Homo mapienm
CDNA clone CS0DB009YC01 5-PRIME, mRNA mequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7238.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
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BX331615.1 GI:30310073
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cgi-bin/cluster.cgi?seq=CSODB009AB01QP1&cluster=7238.f. Contact Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
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BP 191 91006 EVRY cedex - France
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BF982158 1098 bp mRNA linear EST 23-07 60230876F1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:4400298 mRNA sequence.
BF982158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="NEUROBLASTOMA COT 10-NORMALIZED" /clone_Tib="Homo sapiens NEUROBLASTOMA COT 10-NORMALIZED" /note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EicR "
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/clone="CSODB009YC01"
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High quality sequence stop: 693.
Location/Qualifiers
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National Institutes of Health, Mammalian Gene Collection (MGC)
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1 (bases 1 to 1098)
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                         1 (bases 1 to 1201)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 15, 2001 this sequence version replaced
                                                                                                                                                                                                                                                                       AL546472 Homo sapiens PLACENTA COT 25-NORM CIONE CSODIO30YJ01 5-PRIME, mRNA sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                         Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="duodenal adenocarcinoma, cell line"
/lab_host="PH10B (phage resistant)"
/clone_lib="NIH MgC_88"
/clone_lib="NIH MgC_88"
/note="forgan: small intestine; Vector: pCMV-SPORT6;
Site_1: NotI; Site_2: Sall; Cloned unidirectionally;
oligo-dT primed. Average insert size 1.767 kb. Library
enriched for full-length clones and constructed by Life
Technologies. Note: this is a NIH_MGC Library."
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/mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                    p mRNA linear EST 31-MAY-200:
COT 25-NORMALIZED Homo sapiens cDNA
                                 gi:12879620
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RESULT 11
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BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7238.f For
more information about this cluster, see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cgi-bin/cluster.cgi?seq=CSODI030CE01QP1&cluster=7238.f. Contact: Feng Liang Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com/ InvitroGen Corporation 1600 Faraday Avenue Genoscope sequence ID: CSODI030CE01QP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        вуву/986 mRNA linear EST 16-AUG-
AGENCOURT_8482480 Lupski_dorsal_root_ganglion Homo sapiens cDNA
clone IMAGE:6185883 5', mRNA sequence.
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                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James R. Lupski
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                              http://image.llnl.gov
Plate: LLAM13577 row: g column: 04
                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                      Unpublished (1999)
                                                                                                                                                found through the I.M.A.G.E. Consortium/LLNL at:
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                                          quality sequence start: 7 quality sequence stop: 277.
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/note="Ist strand cDNA was praced with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODI030YJ01"
Location/Qualifiers
1. .1222
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TITLE
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                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
Tissue Procurement: Kristi A. Egland, Ira Pastan
Tissue Procurement: Kristi A. Egland, Ira Pastan
CDNA Library Preparation: Invitrogen Corp
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM14279 row: j column: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 924)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
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CA488543.1
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                                                                                                                                         High quality sequence stop: 637.
Location/Qualifiers
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/organism="Homo sapiens"
/mol type="mRNA"
/db_xref="taxon:9606"
/clone="TMAGE:6720309"
/cell_line="ZR-75-1, MCF7,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clome lib="Lupski dorsal root ganglion"
/note="Vector: pCMV-SPORT6 (Life Technologies); Sit
Not1; Site 2: Sal1; cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:
5'-TCGACCCACGCGTCCG-3' and
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/dev_stage="adult, 36 yr"
/lab_host="DHIOB"
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/mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 1077)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
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cgi-bin/cluster.cgi?seq=CSODL004CH02QP1&cluster=7238.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :
Feng Liang Email : fliang@lifetech.com Corporation 1600
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 1077)
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/clone_lib="MAPCL"
/clone_lib="MAPCL"
/note="Wecttor: pcWv-SPORT6; Site_1: EcoRV; Site_2: Not I;
/note="Wecttor: pcWv-SPORT6; Site_1: EcoRV; Site_2: Not I;
/note="Wecttor: pcWv-SPORT6; Site_1: EcoRV; Site_2: Not I;
/note="Wecttor: pcwv-SPORT6; Site_1: Side_2: Not I;
/note="Wecttor: pcwv-SPORT6; Site_1: Side_2: Note I;
/note="Wecttor: pcwv-SPORT6; Site_1: Site_2: Note I;
/note="Wecttor: pcww-SPORT6; Site_1: Site_2: Note I;
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/note="Wecttor: pcww-SPORT6; Site_1: Discorv; Site_2: Note I;
/note-pcww-SPORT6; Site_1: Discorv; Sit
/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pcMVSPORT 6 vector. Library was normalized
                                                                                                                                                                 /clone lib="Homo sapiens B CELLS (RAMOS CELL LINE)
25-NORMALIZED"
                                                                                                                                                                                                                                                 /clone="CSODL004YP03"
/cell_type="B CELLS (RAMOS CELL LINE) COT 25-NORWALIZED'
/cell_line="RAMOS CELL LINE"
                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                        'db_xref="taxon:9606"
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CELLS (RAMOS CELL LINE) COT 25-NORMALIZED
CSODL004YP03 5-PRIME, mRNA sequence.
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Percent Similarity:

0.00152 127.00 96.43%

Length: Matches: Conservative:

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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BF977311 589 bp mRNA linear EST 22-JA 60214648551 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4305501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tissue Procurement: ATCC/DCTD/DTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        quality sequence stop: 586.
                                  /tissue_type="melanotic melanoma, high MDR"
/lab_host="DH10B (Ti phage-resistant)"
/clone_lib="NIH_MGC_62"
/clone_lib="NIH_MGC_62"
/clone_lib="NIH_MGC_62"
/clone_lib="skin; Vector: pDNR-LIB (Clontech); Site_1:
/sfil (ggccgcttcggcc); Site_2: Sfil (ggccattatggcc);
Sfil (ggccgcttcggcc); Site_2: Sfil (ggccattatggcc);
Double-stranded cDNA was prepared from cell line RNA. 5/
and 3/ adaptors were used in cloning as follows: 5/
adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor
sequence: 5'-ATTCTACAGGCCGAGGGCGCCACATC-dT(30)BN-3'
(where B = A, C, or G and N = A, C, or G, or T). Average
insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4305501"
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                         Laboratories (Palo Alto,
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Pred. No.:
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                       Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CA397574 S55 bp mRNA linear EST 06-NOV-2: cs92h10.y2 Human Retinal pigment epithelium/choroid cDNA (Un-normalized, unamplified): cs Homo sapiens cDNA clone cs92h10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6/331, NIH, Bethes
Tel: 301 402 3452
Fax: 301 496 0078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wistow,G., Bernstein,S.L., Wyatt,M.K., Farris,R.N., Behal,A., Touchman,J.W., Bouffard,G., Smith,D. and Peterson,K. Expressed sequence tag analysis of human RPE/choroid for the NEIBank Project: Over 6000 non-redundant transcripts, novel genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
1 (bases 1 to 555)
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CA397574
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              te: 92 row: h column: 10
primer: M13RP1 reverse primer
Location/Qualifiers
                                                                            /clone lib=Human Retinal pigment epithelium/choroid cDNA (Un-normalized, unamplified): cg"
/mote="Organ: Eye; Vector: pcMVSPORT6; Two different donor eyes (75-80 years old) yielded approximately 600 mg of dissected RPE/choroid tissue. This in turn yielded 340 ug of total RNA and 7 ug of mRNA. A directionally cloned cDNA library in the pcMVSPORT6 vector was constructed at Life Technologies (Rockville, MD; now part of Invitrogen Corp), essentially following the protocols of the SuperScript Plasmid System (Invitrogen Corp). chttp://www.invitrogen.com/>). The library code designation was cs. For this library, cDNA inserts were cloned into the Notl/MJU sites of the vector. EST analysis was performed on the unamplified library at the NIH Intramural Sequencing Center (NISC)."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     graeme@helix.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="RPE/choroid"
/dev_stage="Adult"
/lab_host="EMDH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="cs92h10"
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Conservative:
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-NCPU=6 -ICGPU=3 -NO_MMAP -LARGEQUERY -NEG SCORES=0 -MAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Delop 6.0 , Delext
is the number of results predicted by chance to have a sater than or equal to the score of the result being printed, rived by analysis of the total score distribution.
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Copyright (c) 1993 - 2004 Compugen Ltd.
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equence 20063	guence 39, App	quence 1, Appli	e 262, A	e 67822	e 6782	e 6782	e 6782	e 6782	6	equence 3076	quence 14095	e 11275,	6089	equence 1269,	16	equence 10,	quence 10,	e 24,	e 1, Appl	equence 1, Appl	e L		23	299	e 65, Ap	equence 65, App	e 7060,	12900,	equence 1,	equence 1, App	e 522	equence	equence 754,	equence 15190	Ñ	equence 2417	Sequence 6, Appli	e 14,	Sequence 13, Appl	13, 1	e 26,	Sequence 26, Appl	equence 1, A	Sequence 1, Appli

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ALIGNMENTS

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NESULT 1

US-09-122-383-1

US-09-122-383-1

Sequence 1, Application US/09122383A

Patent No. US20020042093A1

APPLICANT: Sheppard, Paul O.
APPLICANT: Gilbertson, Debra G.
TITLE OF INVENTION: SECRETED PROTEINS ENCODED BY HUMAN
TITLE OF INVENTION: HOMOSOME 13

FILE REFERENCE: 97-38

CURRENT APPLICATION NUMBER: US/09/122,383A

CURRENT FILING DATE: 1998-07-24

EARLIER APPLICATION NUMBER: 60/053,613

EARLIER OF SEQ ID NOS: 19

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 1

SEQ ID NO 1
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Result

Score

Query Match Length DB

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Description

SUMMARIES

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WESULT 3
US-10-633-595-26
; Sequence 26, Application US/10653595
; Publication No. US20040048304A1
; GRNERAL INFORMATION:
; APPLICANT: Ruben et. al.
; TITLE OF INVENTION: 95 Human secreted proteins
; FILE REFERENCE: PZ027P1C1
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US-10-010-050A-1
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SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1486
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Publication No. US20020173624A1
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APPLICANT: Gilberteson, Debra G.
APPLICANT: Gilberteson, Debra G.
TITLE OF INVENTION: SECRETED PROTEINS ENCODED BY HUMAN
TITLE OF INVENTION: CHROMOSOME 13
FILE REFERENCE: 97-38C1
CURRENT APPLICATION NUMBER: US/10/010,050A
CURRENT FILING DATE: 2002-03-26
PRIOR APPLICATION NUMBER: US 09/122,383
PRIOR PILING DATE: 1998-07-24
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NAME/KEY: CDS
LOCATION: (47)...(1084)
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ORGANISM: Homo
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CURRENT FILING DATE: 2003-09-03
PRIOR APPLICATION NUMBER: US 09/397945
PRIOR FILING DATE: 1999-03-18
PRIOR APPLICATION NUMBER: PCT/US99/05804
PRIOR APPLICATION NUMBER: 60/078,566
PRIOR PILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/078,576
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/078,573
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/078,574
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/078,574
PRIOR APPLICATION NUMBER: 60/078,579
PRIOR APPLICATION NUMBER: 60/078,578
PRIOR PILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/078,578
PRIOR PILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/078,578
PRIOR FILING DATE: 1998-04-01
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LENGTH: 1751
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ORGANISM: Homo sapiens
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NAME/KEY: SITE
LOCATION: (1741)
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OTHER INFORMATION:
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JS-10-010-050A-2_COPY_1_28 (1-28)
                                                                    Best Local Similarity:
                                                                                         Percent Similarity:
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JS-09-397-945-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Ver. SEQ ID NO 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 1998-04
NUMBER OF SEQ ID NOS: 470
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PRIOR APPLICATION NUMBER: 60/078,574
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PRIOR FILING DATE: 1999-03-18
PRIOR APPLICATION NUMBER: 60/078,566
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CURRENT FILING DATE: 1999-09-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/080,313
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                                                                                                                                                                                                                              LOCATION: (1735)
OTHER INFORMATION:
NAME/KEY: SITE
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OTHER INFORMATION:
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LOCATION: (1689
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NAME/KEY: SITE
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FILING DATE: 1998-03-19
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APPLICATION NUMBER: 60/078,578
FILING DATE: 1998-03-19
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Best Local Similarity:
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Publication No. US20020173624A1
GENERAL INFORMATION:
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LENGTH: 1038
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                                                       CURRENT APPLICATION NUMBER: US/10/010,050A GURRENT FILING DATE: 2002-03-26 PRIOR APPLICATION NUMBER: US 09/122,383 PRIOR FILING DATE: 1998-07-24 PRIOR APPLICATION NUMBER: US 60/053,613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT FILING DATE: 1998-07-24
EARLIER APPLICATION NUMBER: 60/053,613
EARLIER FILING DATE: 1997-07-24
NUMBER OF SEQ ID NOS: 19
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TITLE OF INVENTION: SECRETED PROTEINS ENCODED
TITLE OF INVENTION: CHROMOSOME 13
FILE REFERENCE: 97-38
CURRENT APPLICATION NUMBER: US/09/122,383A
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                                                                                                                                                                                    APPLICANT: Sheppard, Paul O.
APPLICANT: Gilbertson, Debra G.
TITLE OF INVENTION: SECRETED PROTEINS ENCODED
TITLE OF INVENTION: CHROMOSOME 13
SOFTWARE: FastSEQ for Windows Version 4.0
                 PRIOR FILING DATE: 1997-07-24
NUMBER OF SEQ ID NOS: 19
                                                                                                                                                                  FILE REFERENCE: 97-38C1
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OTHER INFORMATION: n is any nucleotide
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NAME/KEY: variation
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US20020042093A1
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; OTHER INFORMATION: n = A, T, C or US-10-010-050A-13
; Sequence 6, Application US/10329079; Publication No. US20030198981A1
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APPLICANT: FARNET, Chris
APPLICANT: ZAZOPOULOS, Emmanuel
APPLICANT: STAFFA, Alfredo
TITLE OF INVENTION: GENES AND PROTEINS INVOLVED IN THE BIOSYNTHESIS OF LIPOPEPTIDES
FILE REFERENCE: 3002-11US
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn version 3.0 SEQ ID NO 14
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CURRENT FILING DATE: 2002-12-24
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                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 7155
TYPE: DNA
ORGANISM: Streptomyces fradiae
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OTHER INFORMATION: polypeptide of SEQ ID NO:2
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ENGTH: 1038
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                                                                                                                      23 LeuAlaVal
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RESULT 9
US-10-027-632-241716
US-10-027-632-241716, Application US/10027632; Sequence 241716, Application US/0027632; Publication No. US20020198371A1
; Publication No. US20020198371A1
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Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR PELICATION NUMBER: US 60/198,676
PRIOR PELICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-02-24
PRIOR PELICATION NUMBER: US 60/167,363
PRIOR PELICATION NUMBER: US 60/167,363
PRIOR PELICATION NUMBER: US 60/167,363
PRIOR PELICATION NUMBER: US 60/156,358
PRIOR PELICATION NUMBER: US 60/156,358
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR PILING DATE: 1999-09-28
PRIOR PELICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-09-28
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Best Local Similarity:
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                                                                           Score:
                                                                                                  Pred. No.:
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                                                                                                                                                                                                                                                                     SEQ ID NO 241716
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APPLICANT: ZAZOPOULOS, Emmanuel
APPLICANT: STAFFA, Alfredo
TITLE OF INVENTION: GENES AND PROTEINS INVOLVED IN THE BIOSYNTHESIS OF LIPOPEPTIDES
FILE REFERENCE: 3002-11US
CURRENT APPLICATION NUMBER: US/10/329,079
CURRENT FILLING DATE: 2002-12-24
NUMBER OF SEQ ID NOS: 66
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
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CURRENT FILING DATE: 2002-04-30
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                                                                                                                                                                                               ORGANISM: Human
                                                                                                                                                                                                                     TYPE: DNA
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Matches:
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Matches:
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Indels:
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CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR PILING DATE: 2000-03-29
PRIOR PILING DATE: 2000-02-24
                                                                                                                           Sequence 15190, Application US/10282122A Publication No. US20040029129A1
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-10-282-122A-15190
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st Local Similarity:
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Publication No. US20030204075A9
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
                                                                                                       BENERAL INFORMATION:
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10-027-632-241716
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
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FILLING DATE: 1999-11-23
APPLICATION NUMBER: US 60/156,358
FILLING DATE: 1999-09-28
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US-10-087-192-754/c
; Sequence 754, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
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Best Local Similarity:
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APPLICANT: Morris, David W.
APPLICANT: Engelhard, Eric K.
APPLICANT: Engelhard, Eric K.
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: CANCER
FILE REFERENCE: 529452000122
CURRENT APPLICATION NUMBER: US/10/087,192
CURRENT FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR PILING DATE: 2000-120-22
PRIOR APPLICATION NUMBER: US 09/798,586
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PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
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PRIOR TILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
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TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.034A
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PRIOR FILING DATE: 2000-03-21
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FILING DATE: 2000-09-06
APPLICATION NUMBER: 60/230,347
FILING DATE: 2000-09-09
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                                                                                                                                                                                                                                                                                                                                            311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wall, Daniel
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Matches:
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Indels:
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S-10-010-050A-2_COPY_1_28 (1-28) x US-10-029-517-106 (1-772)
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                                                        Sequence 5227, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                             est Local Similarity:
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LENGTH: 772
TYPE: DNA
ORGANISM: Homo s
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Best Local Similarity:
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            APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, Davi
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Publication No. US20030148969A1
GENERAL INFORMATION:
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NUMBER OF SEQ ID NOS: 2059
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 754
LENGTH: 276276
TYPE: DNA
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CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Kenneth W. Dobie
APPLICANT: Susan J. Myers
TITLE OF INVENTION: ANTISENSE MODULATION OF MUCIN 1, TRANSMEMBRANE EXPRESSION
FILE REFERENCE: RTS-0352
                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
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Zhou, Yīhua
Kovalic, David I
Screen, Steven J
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Best Local Similarity:
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DB:
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NAME/KEY: misc feature
LOCATION: (1)...(322101

TANDARMATION: n =
                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Gudmundsson Gudmundur
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/10354247
Publication No. US20030224393A1
                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/354,247
COURRENT FILING DATE: 2003-01-29
PRIOR APPLICATION NUMBER: US 10/060,902
PRIOR FILING DATE: 2002-01-30
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 5227
LENGTH: 1257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: GENE FOR PERIPHERAL ARTERIAL OCCLUSIVE FILE REFERENCE: 2345.2012-003
                                                                                                                                                                                                                                                                     OTHER INFORMATION: n = A,T,C
                                                                                                                                                                                                                                                                                                                                        LENGTH: 322101
TYPE: DNA
ORGANISM: Homo sapiens
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Search completed: April 25, Job time: 95.8056 secs

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Command line parameters:

-MODEL=frame+_D2n.model - DEV=xlh
-MODEL=frame+_D2n.model - DEV=xlh
-Q=(cgn2_1/USPTO_spool/US10010050/runat_22042004_113205_27569/app_query.fasta_1.1372
-DB=fssued_Patents_NA -QFMT=fastap_-SUFFIX=rni -MINMATCH=0.1 -LODECL=0
-LODEXT=0 -UNITS=5its -START=1 -RNO=1 - MARIX=blosum62 -FRANS=human40.cdi
-LIST=45 -DCCALIGNE200 -THR_SCORE-pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM-ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10010050 @CGN 1 1 140 @runat_22042004 113205_27569 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPEXT=0 -XGAPEXT=0.5 -FGAPOP=6
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Fgapop 6.0 , F
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US-09-385-707-7
US-09-439-923-1
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US-09-39-696A-6
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equence 9, Appl	e 7	Sequence 5, Appli	e ა	e 1,	e 4,	е 4,	e 50	Φ	e 831,	e 831,	e 831	e 11793,	e 1,	e 4, Appl	e 5, Appl	11216,	e 11039,	25, Ap	1121, A	3, Appl	equence 2, Appl	e 22 -	e 1161, Ā	equence 688, Ap	e 738, F	ው	e 5264,	nce 5631,	e 2735,	nce 2986, A	equence 2, Ap	Sequence 11459, A

ALIGNMENTS

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RESULT 1
US-08-713-928B-8/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: CRADIN, DAVID N.
APPLICANT: CRADER, CAROLE L.
APPLICANT: OISHI KAREN K.
APPLICANT: WEISSNBORN, DEBORAH L.
APPLICANT: WEISSNBORN, DEBORAH L.
TITLE OF INVENTION: PLANT-BASED EXPRESSION SYSTEMS
TITLE OF INVENTION: PLANT-BASED EXPRESSION SYSTEMS
                                                                               APPLICATION NUMBER: US/08/713,928B FILING DATE: 13-SEP-1996 CLASSIFICATION: 800 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 60/003,737 FILING DATE: 14-SEP-1995 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/713,928B
                                                                                                                                                                                                                                                                                                                               ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
TELECOMMUNICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
              NAME: Coruzzi, Laura A. REGISTRATION NUMBER: 30 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 1155 Avenue of CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                          New York
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INFORMATION:
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TELEPHONE:

(212) 869-9741

(212) 790-9090

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RESULT 2
US-09-191-171-4/c
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Query Match:
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Patent No. 6149909 6143294
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/09191171
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                                                                         PRIOR APPLICATION NUMBER: US 08/494,104
FILING DATE: 23-UN-1995
APPLICATION NUMBER: AU PK9490/91
FILING DATE: 14-NOV-1991
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 2067 base pair
                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARB: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/191,171
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
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                                PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: SCULLY SCOTT MURPHY & PRESSER STREET: 400 Garden City Plaza CITY: Garden City
                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                APPLICATION NUMBER: AU PCT/AU92/00611 FILING DATE: 12-NOV-1992
                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                            STATE: New York
               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE:
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DEDNESS: unknown
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MORRIS, Charles P.

HOPMOOD, John J.

VENTION: SYNTHETIC ALPHA-L-IDURONIDASE AND GENETIC

VENTION: SEQUENCES ENCODING SAME
                                                                                                                                                                                                                                                                                                                                                                             USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORSBORN, Annet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANSON,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SCOTT, Hamish S. ANSON, Donald S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                unknown
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07-JUL-1993
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62.50
48.28%
44.83%
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             US 08/084,254
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Matches:
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Indels:
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 3
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US-09-191-171-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: DiGigllo, rram, 1,346
REGISTRATION NUMBER: 8978
REFERENCE/DOCKET NUMBER: 8978
TELECOMMUNICATION INFORMATION:
TELEPHONE: 516-742-4343
TELEPAX: 516-742-4366
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                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                             COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/385,707
                                                                                                                                                                              ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: SCULLY SCOTT MURPHY & PRESSER
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
                              PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                      APPLICANT: CLEMENTS, Peter R.
APPLICANT: MORRIS, Charles P.
APPLICANT: HOPWOOD, John J.
TITLE OF INVENTION: SYNTHETIC ALPHA-L-IDURONIDASE AND GENETIC
TITLE OF INVENTION: SEQUENCES ENCODING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
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ATTORNEY/AGENT INFORMATION
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                                                               CLASSIFICATION:
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6238662
Watti
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                                                                                                                                                                                                                                      USA
                                                                                                                                                                                                                                                                                                                                                                                                                                           ORSBORN, Annette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SCOTT, Hamish S. ANSON, Donald S.
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                                08/494,104
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Indels:
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Matches:
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KEGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 897
TELECOMMUNICATION INFORMATION:

8978Z

NAME: DiGiglio, Frank S. REGISTRATION NUMBER: 31,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/09639696C Patent No. 6524835 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        . No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 2155 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY:
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TELEFAX: 516-742-4366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION:
           APPLICATION NUMBER: US/09/639,696C
FILING DATE: 16-Aug-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/191,171
FILING DATE: 13-NOV-1998
APPLICATION NUMBER: US 08/494,104
                                                                                                                                           COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                         HOPWOOD, John J.
TITLE OF INVENTION: SYNTHETIC ALPHA-L-IDURONIDASE AND GENETIC SEQUENCES ENCODING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1109
                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON PEABODY LLP
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                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
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STATE: New York
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FILING DATE: 23-JUN-1995
                                                                                                                                                                                                                                                                                 COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                    STREET: 990 Stewart Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   89..2047
                                                                                                                                                                                                                                                                 11530
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NELSON, Paul V.
CLEMENTS, Peter R.
MORRIS, Charles P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SCOTT, Hamish
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62.50
48.28%
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Donald S.
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 7, Application Us, Patent No. 6149909
Patent No. 6149909 6143294
                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORM
APPLICANT: 4
APPLICANT: 4
APPLICANT: 4
      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC comparible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                APPLICANT: ORSBORN, Annette M.
APPLICANT: NELSON, Paul V.
APPLICANT: CLEMENTS, Peter R.
APPLICANT: MORRIS, Charles P.
APPLICANT: HOPWCOD, John J.
TITLE OF INVENTION: SYNTHETIC ALPHA-L-IDURONIDASE AND GENETIC TITLE OF INVENTION: SEQUENCES ENCODING SAME
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
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FILING DATE: 14-NOV-1991
APPLICATION NUMBER: AU PCT/AU92/00611
FILING DATE: 12-NOV-1992
APPLICATION NUMBER: US 08/084,254
FILING DATE: 07-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: POKABISKY, Ann R.
REGISTRATION NUMBER: 34,697
REFERENCE/DOCKET NUMBER: 2249/304
                                                                                                                                              ADDRESSEE: SCHLLY SCOTT MURPHY & PRESSER STREET: 400 Garden City Plaza CITY: Garden City STATE: New York
                                                                                                               ZIP: 11530
                                                                                                                                COUNTRY:
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TELEPHONE: 516-832-7572
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LOCATION:
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TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                  USA
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44.83%
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62.50
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Matches:
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PRIOR APPLICATION DATA:

US 08/494,104

US/09/191,171

CLASSIFICATION: APPLICATION NUMBER: FILING DATE:

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Best Local Similarity:
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Patent No. 6238662
GENERAL INFORMATI
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TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO:
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APPLICANT:
APPLICANT:
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No.:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08
FILING DATE: 07-JUL-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: DiGiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 89
TELECOMMUNICATION INFORMATION:
TELEPHONE: 516-742-4343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PCT/AU92/00611
FILING DATE: 12-NOV-1992
                                                                                                                                                       APPLICANT: MORRIS, Charles P.
APPLICANT: HOPMOOD, John J.
TITLE OF INVENTION: SYNTHETIC ALPHA-L-IDURONIDASE AND GENETIC
TITLE OF INVENTION: SEQUENCES ENCODING SAME
NUMBER OF SEQUENCES: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                     APPLICANT:
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TOPOLOGY: lir
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                         STREET:
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                                                   COUNTRY:
                                                                                                                           ADDRESSEE:
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                                    11530
                                                                    Garden City
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                                                                                                                                                                                                                                                                                                                                                                           Application US/09385707
                                                                                                       E: SCULLY SCOTT MURPHY & PRESSER
                                                       USA
                                                                                                                                                                                                                                                                    ORSBORN, Annette M. NELSON, Paul V.
                                                                                                                                                                                                                               CLEMENTS, Peter R. MORRIS, Charles P.
                                                                                                                                                                                                                                                                                                     SCOTT, Hamish S. ANSON, Donald S.
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Matches:
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Best Local Similarity:
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                                                          Alignment Scores:
  Percent Similarity:
                                                                                                   US-09-439-923-1
                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/09439923

Patent No. 6425208

GENERAL INFORMATION:
APPLICANT: Emil D. Kakkis
APPLICANT: Emil D. Kakkis
APPLICANT: Becky Tanamachi
TITLE OF INVENTION: Recombinant Alpha-L-Iduronidase, Methods
TITLE OF INVENTION: For Producing and Purifying the Same and
TITLE OF INVENTION: Treating Diseases Caused by Deficiencies
FILE REFERENCE: 08000051US00
                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1
LENGTH: 6200
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TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/439,923
CURRENT FILING DATE: 1999-11-12
                                                                                                                                                       TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                  NAME/KEY: CDS
LOCATION: (1558)...(3516)
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LENGTH: 4480 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/385,707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 89
TELECOMMUNICATION INFORMATION:
TELEPHONE: 516-742-4343
TELEPHAX: 516-742-4366
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ATTORNEY/AGENT INFORMATION:
NAME: DIGIGILO, Frank S.
REGISTRATION NUMBER: 31,
                                       No
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
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48.28%
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537
62.50
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Length:
Matches:
Conservative:
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Matches:
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APPLICANT: Emil D. Kakkis
APPLICANT: Becky Tanamachi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence 1, Application US/09711202A
Patent No. 6569661
                                                                                                                                                                                                                   Sequence 1, Application US/09711205A Patent No. 6585971
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Recombinant Alpha-L-Iduronidase, Methods
TITLE OF INVENTION: for Producing and Purifying the Same and Methods for
TITLE OF INVENTION: Treating Diseases Caused by Deficiencies Thereof
FILE REFERENCE: 08000051US00
CURRENT APPLICATION NUMBER: US/09/711,202A
CURRENT FILING DATE: 2000-11-09
PRIOR APPLICATION NUMBER: US/09/439,923
PRIOR APPLICATION NUMBER: US/09/439,923
PRIOR FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 2
APPLICANT: Emil D. Kakkis
APPLICANT: Becky Tanamachi
ITILE OF INVENTION: Recombinant Alpha-L-Iduronidase, Methods
TITLE OF INVENTION: For Producing and Purifying the Same and Methods for
TITLE OF INVENTION: Treating Diseases Caused by Deficiencies Thereof
FILE REFERENCE: 08000051US00
CURRENT APPLICATION NUMBER: US/09/711,205A
CURRENT FILING DATE: 2000-11-09
PRIOR APPLICATION NUMBER: US/09/439,923
PRIOR FILING DATE: 1999-11-12
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LOCATION: (1558)...(3516)
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TYPE: DNA
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Indels:
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alignment Scores:
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LOCATION: (1558)...(3516)
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TYPE: DNA
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                                                                                                                                                                                                                                                   SOPTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/09/639,696C
FILING DATE: 16-Aug-2000
                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
FILING DATE: 07-JUL-1993 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON PEABODY LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HOPWOOD, John J.
TITLE OF INVENTION: SYNTHETIC ALPHA-L-IDURONIDASE AND GENETIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: SCOTT, Hamish
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2638 CGAAGGGGTGCGGGTAGCTCAGGAAGGCATTGTCGTTGCTCAGGAGCGCGTAGGGGA 2579
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                                                     APPLICATION NUMBER: US 09/191,171
FILING DATE: 13.NOV-1998
APPLICATION NUMBER: US 08/494,104
FILING DATE: 23.JUN-1995
APPLICATION NUMBER: AU PK9490/91
FILING DATE: 14.NOV-1991
APPLICATION NUMBER: AU PCT/AU92/00611
APPLICATION NUMBER: AU PCT/AU92/00611
FILING DATE: 12.NOV-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ArgArgGlyAla-----
                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Garden City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 990 Stewart Avenue
                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 11530
                                    APPLICATION NUMBER: US 08/084,254
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                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/676,610B
CURRENT FILING DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 182
SEQ ID NO 24
LENGTH: 169998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Jacqueline Wyatt
APPLICANT: Susan M. Freier
TITLE OF INVENTION: OLICONUCLECTIDE INHIBITION OF HER-1 EXPRESSION
FILE REFERENCE: RTS-0138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 24, Application US/09676610B
Patent No. 6444465
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LOCATION:
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NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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REFERENCE/DOCKET NUMBER: 2249/304
TELECOMMUNICATION INFORMATION:
TELEPHONE: 516-832-7572
TELEFAX: 516-832-7555
INFORMATION FOR SEQ ID NO: 6:
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LENGTH: 6238 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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21 LeuTrpLeuAlaValValProGly 28

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US-09-621-976-11459/c
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APPLICANT: K. Danenberg
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                                                                                                                                                                                                                                                                                                                   SEQ ID NO 11459
LENGTH: 365
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No. 6639063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Method of determining Epidermal Growth
TITLE OF INVENTION: Factor Receptor and HER2-Neu Gene Expression
TITLE OF INVENTION: and Correlation of Levels Thereof With Survival
FILE REFERENCE: 11220/120
CURRENT APPLICATION NUMBER: US/09/877,177A
CURRENT FILING DATE: 2001-06-11
                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
EILE REFERENCE: GENGST.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
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SOFTWARE: Patent.pm
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ORGANISM: Homo sapiens
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SEQ ID NO 2986
LENCTH: 657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence 2, Application US/09069023A Patent No. 6348573
                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2986, Application US/09489039A Patent No. 6610836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Nunez, Gabriel
APPLICANT: Inohara, Naohiro
APPLICANT: Inohara, Naohiro
APPLICANT: Koseki, Takeyoshi
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS
FILE REFERENCE: UM-03333
CURRENT APPLICATION NUMBER: US/09/069,023A
CURRENT FILING DATE: 1998-04-27
NUMBER OF SEQ ID NOS: 38
CURRENT OF SEQ ID NOS: 38
                                                                                                                                                                                                                                                 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TITLE OF INVENTION: PNEUMONLAE FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: 2709.2004001

CURRENT APPLICATION NUMBER: US/09/489,039A

CURRENT FILING DATE: 2000-01-27

PRIOR APPLICATION NUMBER: US 60/117,747

PRIOR APPLICATION NUMBER: US 60/117,747
                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                            ORGANISM: Klebsiella
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DB=N Geneseq_29Jan04 -OFMT=fastap -SUFFIX=rng -MINMATCH=0.1 -LODECL=0

LODEXT=0 -UNITS=bits -START=1 -END=1 - HARTX=blosum62 -TRANS=human40.cdi

LIST=45 -DCCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN-0 -ALIGN=15

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Aak92158 Human cDN
Aax02855 Human zsi
Aaz24826 Human sec
Aak94829 Human ful
Abg40653 Oligonucl
Abg40652 Oligonucl
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2000JP-00118774
2000JP-00183765
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830 Primers useful for synthesizing full length cDNA clones and their use

WPI; 2001-524255/58.

Ota T,

(HELI-) HELIX RES INST.

Wakamatsu

Nishikawa T,] su A, Sugiyama

Isogai T, ma T, Nagai

Hayashi K, i K, Kojima

ŝ Ishii S, S, Otsuki

Kawai T, Ko ĸ,

in genetic manipulation

SEQ

ID NO 1884; 1380pp + Sequence Listing; English.

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       Claim 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; full length cDNA; cDNA synthesis; oligo-capping; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence was used as the representative sequence from a human clone which was used in homology searches to identify the clone. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from
                                                                         830 Primers useful for synthesizing full length
                                                                                                                             WPI; 2001-524255/58.
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K, Kojima
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New secreted polypeptide, zsig46, and its fragments,

related fusion

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                                        WPI; 1999-142930/12.
P-PSDB; AAW92967.
                                                                                                            Sheppard
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                                                                                                                                                                                                                                            24-JUL-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Secreted protein; zsig46; human; chromosome 13; thyroid; disea hypothyroidism; Graves' disease; thyrotoxicosis; thyroid cance Hirschsprung's disease; neuronal ceroid-lipofucinosis; Wilson Reiger syndrome; immunoassay; detection; anti-idiotypic antibo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the ollop-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is the nucleotide sequence of the 5'-end of a cDNA provided in the invention. Note: The sequence data for this patent and the first control of the sequence of th
                                                                                                                                                       (ZYMO ) ZYMOGENETICS
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RESULT 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia, developmental abnormality; foetal deficiency; blood; allergy; renal; ds; immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
                                                                                                                                                                                                                                                                                                                                                 cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus; osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion; endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
                               19-MAR-1998;
19-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               syndrome). Antibodies and other binding proteins, are used as immunoassay reagents to detect zsig46 or cells expressing it, e.g. for assessing thyroid function to produce anti-idiotypic antibodies, for affinity purification of zsig46, to screen expression libraries, to neutralise zsig46 activity, and to deliver toxins, radioisotopes etc. for therapeutic or diagnostic purposes Agonists of the product can be used to promote growth, differentiation and proliferation of specific cell types, e.g. for treating (extra)thyroid diseases or as additive to cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention describes the isolation of a novel human secreted protein, zsig46 encoded by a gene on chromosome 13 which is mainly expressed in the thyroid. This product can be used to study secretion of proteins from cells and also to treat or prevent deficient expression of zsig46, which may be associated with thyroid diseases (e.g. hypothyroidism, Graves' disease, thyrotoxicosis, thyroid cancer etc.) or with diseases that involve genes in the same region of chromosome 13 (e.g. Hirschsprung's disease, neuronal ceroid-lipofucinosis, Wilson disease and Reiger
                                                                                                                                                                                  23-SEP-1999.
                                                                                                                                                                                                                                             WO9947540-A1.
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    used for diagnosis and treatment

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98US-0078563P.
98US-0078566P.
98US-0078573P.
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                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence represents a nucleic acid molecule which encodes a secreted human protein. The gene number, and the clone it is derived from, are detailed in the descriptor line. The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin Fc portion (e.g. AAZ24802) for increasing the stability of the fused protein as compared to the human protein only. The invention relates to 95 novel genes and their fragments (nucleic acid sequences: AAZ24811-Z24907; amino acid sequences AAY41308-Y41404) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the amount of the new polynucleotides. Specific uses are described for each of the 95 polynucleotides, based on which tissues they are most highly expressed in (see AAZ24811 for described uses)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-MAR-1998;
19-MAR-1998;
19-MAR-1998;
19-MAR-1998;
19-MAR-1998;
19-MAR-1998;
01-APR-1998;
01-APR-1998;
                      Human; full length
                                                Human
                                                                         06-NOV-2001
                                                                                                                           AAK94829
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1751 BP;
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                                                                                                                                                                                                                                                                                                                                                                      No.:
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                                             full-length cDNA, SEQ ID NO: 3977
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                                                                                                                          standard; cDNA;
                                                                                                                                                                                              LeuTrpLeuAlaValProGly 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Page
                                                                                                                                                                                                                            ATGCGGCGGGCGGGCGCGCTCCGGGGACGCGCTTCCTGGTGCTGGGCCCCTGGCGCTTG
                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               308; 484pp; English.
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                  cDNA; cDNA synthesis; oligo-capping; ss.
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RESULT 6
ABQ40653/c
ID ABQ406
XX ABQ406
XX ABQ406
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XX Oligon
XX Oligon
XX Human;
KW drug;
KW drug;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cINA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA esaily without any special methods. The present sequence is a full length human cDNA of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from EPO
                            Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis; drug; side effect; cancer; central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphism SNP; cell differentiation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 8; SEQ ID NO 3977; 1380pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    830 Primers useful for synthesizing full length cDNA clones and their use
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11-JAN-2000; 2000JP-00118774.
02-MAY-2000; 2000JP-00183765.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to primers for synthesising full length
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                                                                                                     Oligonucleotide for detecting cytosine methylation SEQ ID NO 27244.
                                                                                                                                      12-JUL-2002
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su A, Sugiyama
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                                                                                                                                                                                                                                                                                      LeuTrpLeuAlaValValProGly 28
                                                                                                                                     (first entry)
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na T, Nagai
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K, Kojima
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                                           nucleotide polymorphism,
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This invention describes a novel method for determining the degree of methylation of a particular cytosine in a motif 5'-CpG-3', present in a genomic sample of DNA. The sample is treated chemically to convert cytosine (c) but not methylated C, to uracil, then part of the genomic DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the degree of hybridisation to both classes is determined from the label on the amplicon. From the ratio of labels hybridised to the two classes of oligomers, the degree of methylation is calculated. The method is used:

(i) for diagnosis and/or prognosis of side effects of therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders of the central nervous, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detacting armitation are contacted.
                                                        particularly by detecting mutations or single nucleotide polymorphisms (SNP'8); and (ii) for differentiation of cell or tissue types and for investigating cell differentiation. The method allows the methylation status of many C residues to be determined simultaneously. ABQ19410-ABQ54121 represent genomic DNA sequences used to illustrate the method for determining the degree of cytosine methylation described in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Determining the degree of cytosine methylation in genomic DNA, useful for diagnosis and prognosis, comprises selective hybridization of amplicons from chemically treated DNA.
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Sequence 630 BP; 219 A; 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 12; 56pp + Sequence Listing; 56pp; German.
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05-SEP-2000;
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2000DE-01044543
                                      the invention
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RESULT 7
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DE Olig
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20 273

Oligonucleotide for detecting cytosine methylation SEQ ID NO 27243.

ABQ40652;

12-JUL-2002

(first entry)

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ABQ13702
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                   ABQ13702 standard; DNA; 631
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-SEP-2000; 2000DE-01043826
05-SEP-2000; 2000DE-01044543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis; drug; side effect; cancer; central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphism; SNP; cell differentiation; ds.
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LeuTrpLeuAlaValValProGly 28

209

ATGCGGCGGGGCGCGGTTCGGGGACGCGTTTTTTTGGTGTTTGGGTTTTTGGCGTTT

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                                                                                                                                                                                                                                        Alignment
                                                                                                                                                                                                                                                                                                                   This invention describes a novel method for determining the degree of comethylation of a particular cytosine in a motif 5'-CpG-3', present in a cytosine in a motif 5'-CpG-3', present in a cytosine (c) but not methylated c, to uracil, then part of the genomic convert con
                                                                                                                                                                        Percent Similarity:
                                                                                                                                                                                                                                                                                 Sequence 631
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05-SEP-2000;
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MetArgArgGlyAlaGlyAlaAlaArgGlyArgAlaSerTrpCysTrpAlaLeuAlaLeu
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2000DE-01044543
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TTTTGGTTCGCGGTGGTTTCGGGT 292

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Best Local Similarity:
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DB:
                                                                                                                           This invention describes a novel method for determining the degree of CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a CC genomic sample of DNA. The sample is treated chemically to convert CC cytosine (C) but not methylated C, to uracil, then part of the genomic CDNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one member, CC disgonacleotides and/or peptide-nucleic acid (PNA) oligomers and the degree of hybridisation to both classes is determined from the label on the amplicon. From the ratio of labels hybridised to the two classes of cligomers, the degree of methylation is calculated. The method is used: (i) for diagnosis and/or prognosis of side effects of therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders of the central construency, cardiovascular, gastrointestinal and respiratory systems etc. particularly by detecting mutations or single nucleotide polymorphisms (SNP's), and (ii) for differentiation. The method allows the methylation curvestigating cell differentiation. The method allows the methylation cancer disconsely. ABQ13110-
CC ABQ54121 represent genomic DNA sequences used to illustrate the method for disconse of the invention.
                                               Percent Similarity:
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)13703/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              drug; side effect; cancer; central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphism; SNP; cell differentiation; ds.
                                                                                                                         Sequence 631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Determining the degree of cytosine methylation in genomic DNA, useful for diagnosis and prognosis, comprises selective hybridization of amplicons
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Best Local Similarity: Query Match:

Percent Similarity:

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Length: Matches:

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                                                                                            This invention describes the isolation of a novel human secreted protein, compared and the product can be used to study secretion of proteins from the thyroid. This product can be used to study secretion of proteins from compared to treat or prevent deficient expression of zsig46, which may be associated with thyroid diseases (e.g. hypothyroidism, Graves' disease, thyrotoxicosis, thyroid cancer etc.) or with diseases that involve genes in the same region of chromosome 13 (e.g. Hirschaprung's compared to the product and the product and the same and the product and the same and the product and isease and Reiger syndrome). Antibodies and other binding proteins, are used as immunoassay creagents to detect zsig46 or cells expressing it, e.g. for assessing thyroid function to produce anti-idiotypic antibodies, for affinity purification of zsig46, to screen expression libraries, to neutralise zsig46 activity, and to deliver toxins, radioisotopes etc. for therapeutic or diagnostic purposes. Agonists of the product can be used to promote growth, differentiation and proliferation of specific cell types, e.g. for treating (extra)thyroid diseases or as additive to cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New secreted polypeptide, zsig46, and its fragments, related fusion proteins - used for diagnosis and treatment of thyroid disorders or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Secreted protein; zsig46; human; chromosome 13; thyroid; disease; hypothyroidism; Graves' disease; thyrotoxicosis; thyroid cancer; Hirschsprung's disease; neuronal ceroid-lipofucinosis; Wilson dis Reiger syndrome; immunoassay; detection; anti-idiotypic antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 31; Page 94-95; 101pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     diseases involving genes on chromosome
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                                                                                    polynucleotides comprising a nucleotide sequence encoding a protein which is involved in or associated with the synthesis, metabolism or degradation of carbohydrates in the plant grain and the expression of which is up-regulated during grain filling. The plant is selected from corn, tomato, banana, canola, cotton, peanut, sorghum, tobacco, sugarbeet, wheat, and rice. The invention may be useful for the improvement of protein, oil, starch, fibre and moisture content of the cereal grains. In addition, carbohydrate levels may be modified to a more desirable level using the present invention. The present sequence is a DNA sequence encoding a rice protein of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New plant genes encoding polypeptides having an activity involved in or associated with the synthesis, metabolism or degradation of carbohydrates in the plant grain useful in generating plants having improved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    plant biotechnology; carbohydrate synthesis; carbohydrate metabolism; carbohydrate degradation; carbohydrate; plant grain; grain filling; corn; tomato; banana; canola; cotton; peanut; sorghum; tobacco; sugarbeet;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nutritional properties.
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Glazebrook J,
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26-SEP-2001; 2001US-0325277P
20-DEC-2001; 2001US-0342327P
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                                                                    ftp.wipo.int/pub/publishedpct_sequences.
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Katagiri F,
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Ricke D;
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Alignment Scores: Pred. No.:

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DB:
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                   The specification describes antisense oligonucleotides (AAX52869-X55271) directed against at least 2 mRNAs selected from target genes, coding and non-coding regions of RNAs corresponding to trarget genes, coding and non-coding regions of RNAs corresponding to trarget genes, gene initiation codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'-end and the juxta-section between coding and non-coding regions and all segments of RNAs encoding proteins associated with one or more diseases, conditions or mixtures. The antisense oligonucleotides may be derived from sequences AAX55272-74. These multiple target oligonucleotides (specifically AAX55180-271) can be used for the antisense treatment of diseases and conditions. Typical diseases and conditions are those associated with impaired respiration and inflammation, including lung diseases, pulmonary vasoconstriction, inflammation, allergic rhinitis, acute asthma, allergies, asthma, impeded respiration, respiratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                acute asthma; allergy; asthma; impeded respiration; respiratory distress syndrome; pain; cystic fibrosis; pulmonary hypertension; pulmonary vasoconstriction; emphysema; chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma; colon cancer; breast cancer; lung cancer; pancreatic cancer;
   distress syndrome,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New antisense oligonucleotides used in treatment of,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 60; 120pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          vasoconstriction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-229400/19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-SEP-1997;
09-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-MAR-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        impaired respiration; inflammation; lung disease; pulmonary vasoconstriction; inflammation; allergic rhinitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Endothelial nitric oxide synthase antisense oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-JUL-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (UYEC-) UNIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        prostate cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antisense oligonucleotide; multiple target; antisense treatment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAX54769
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EAST CAROLINA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry
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98US-00093972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98WO-US019419
   pain, cystic fibrosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA;
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Indels:
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Conservative:
   pulmonary hypertension,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0 0 1 2 2
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DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
oligonucleotide (ON) with low adenosine (up to 15%), which target nucleic acids involved in bronchoconstriction, allergies, and/or inflammation. The ON can have antiinflammatory, antiallergic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity:
                                                                                                                                                    New antisense oligonucleotides useful for treating e.g. pulmonary vasoconstruction, inflammation, allergies, asthma, hypertension,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway; lung disease; ischaemic condition; pulmonary vasoconstriction; asthma; respiratory distress syndrome; pain; cytoic fibroais; emphysema; pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary disease (COPD), and cancers such as leukentas, lymphomas, carcinomas e.colon cancer, breast cancer, lung cancer, pancreatic cancer, hepatic metastasses, hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastasses, well as all types of cancers which may metastasize or have metastasized well as all types of cancers which may metastasize or have
                                                                                   Disclosure; Page 504-505; 1343pp; English
                                                                                                                                      bronchitis, emphysema,
                                                                                                                                                                                                       WPI; 2000-205971/18.
                                                                                                                                                                                                                                                                                                            03-AUG-1998;
                                                                                                                                                                                                                                                                                                                                            03-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                               WO200009525-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antiallergic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          phosphorothioate; impaired respiration; inflammation; allergy;
allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; adenosine receptor; low adenosine antisense oligonucleotide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human adenosine receptor related polynucleotide SEQ ID NO:1905.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAA34216;
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                                                                                                                                                                                                                                                                          (UYEC-) UNIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the lungs, including breast and prostate cancer
                                                   present invention describes a new composition comprising an antisense
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             leukaemia; lymphoma; carcinoma; metastasis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCGGTTGCCCCG 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GlyAlaGlyAlaAlaArgGlyArgAlaSerTrpCysTrpAlaLeuAlaLeuLeuTrpLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AlaValValPro
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                                                                                                                                                                                                                                                                          EAST CAROLINA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                            98US-0095212P
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                                                                                                                                      respiratory distress
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                740 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            x AAX54769 (1-2028)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                792 G; 484 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches:
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                                                                                                                                      syndrome,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0 U; 4 Other;
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                                                                                                                                      ischemia or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                           surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS; respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis; pulmonary hypertension; emphysema; pulmonary transplantation rejection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAF20338;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nucleotide sequences given in the sequence listing from the present invention, which correspond to SEQ ID NO:1 to 2815, and then the last 1 sequences are also called SEQ ID NO:1 to 185, but the sequences differ from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to AAA33992) are specifically claimed ONs from the present invention. N.B. Sequences given in the disclosure of the present invention do not match up with their corresponding SEQ ID NO: sequences given in the sequence
                                                                                                                                                                   26-OCT-2000.
                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                      chronic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic,
respiratory obstruction; pulmonary obstruction; impeded respiration;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     surfactant depletion; respiratory; bronchodilator; antiinflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Low adenosine antisense oligonucleotide; phosphorothicate; allergy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human endothelial nitric oxide synthase polynucleotide fragment #1905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-MAR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                  obstructive pulmonary disease; pulmonary infection; bronchitis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 disorder; bronchoconstriction; lung inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ВP;
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06-APR-1999;

24-MAR-2000; 2000WO-US008020.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      immunoglobulins and antibodies, antibody receptors, cytokines and chemokines, endogenously produced specific and non-specific enzymes, binding proteins, adhesion molecules and their receptors, cytokine and chemokine receptors, adenosine receptors, bradykinin receptors, central nervous system (CNS) and peripheral nervous and non-nervous system receptors, CNS and peripheral nervous and non-nervous system peptide transmitters, defensins, growth factors, vasoactive peptides and receptors, binding proteins and malignancy associated proteins. The antisense oligonucleotides may be used in this way to treat disorders including respiratory obstruction (especially pulmonary obstruction and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or surfactant hypoproduction which are associated with a disease or condition analected from nollmonary vasoconstriction, inflammation, inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity:
Human endothelial nitric oxide synthase antisense fragment no.1892.
                                                                                                                   17-0CT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                condition selected from pulmonary vasoconstriction, inflammation, allergies, asthma, impeded respiration, respiratory distress syndrome (RDS), pain, cystic fibrosis (CF), allergic rhimitis (AR), pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD), pulmonary transplantation rejection, pulmonary infections, bronchitis, and/or cancer. AAF18434 to AAF21543 represent human polynucleotide fragments and antisense oligonucleotides used in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Immunosuppressive, antiasthmatic, hypotensive and cytostatic activities. The antisense oligonuclectides and (I) can be used to down-regulate the expression and or activity of target polypeptides associated with lung/respiratory disorders and maliaments.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Low adenosine (A) content antisense oligonucleotides which do not trigger adenosine receptors during metabolism, useful e.g. for treating cancers and respiratory obstructions.
                                                                                                                                                                                                                                                                                                       ABZ96032 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     lung/respiratory disorders and malignancies, such as stimulating and activating peptide factors and transmitters, transcription factors,
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WANTED TO THE CONTRACT OF THE 
                                                     junctions of genes encoding a polypeptide associated with lung and/or constant airway dysfunction and a second active agent comprising an ansal airway dysfunction and a second active agent comprising an contininflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory, antiallergic, antiasthmatic, hypotensive, considering and cytostatic activity. The composition may have a use in antisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an antiinflammatory steroid in a subject, for reducing or depleting levels of, or reducing sensitivity to adenosine, reducing levels of adenosine receptor, producing bronchodilation, increasing levels of ubiquinone or lung surfactant in a subject's tissue, or treating bronchoconstriction, consignification, lung allergies, or a respiratory disease or condition. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at figure in the printed specification, but was obtained pot_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nyce JW,
Miller S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; antisense; lung dysfunction; nasal airway dysfunction; antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic; antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy; antisense gene therapy; respiratory; lung; adenosine sensitivity; antisense gene thorapy; respiratory; lung; adenosine sensitivity; adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             first active agent comprising an oligonucleotide antisense to the initiation codon, coding region, 5' or 3' end genomic flanking region, 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; SEQ ID NO 11274; 872pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-APR-2001; 2001US-0286137P
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Ś 뭉 á US-10-010-050A-2_COPY_1_28 (1-28) x Best Local Similarity: Score: Alignment Scores: Query Match: Percent Similarity: Pred. No.: 24 AlavalValPro 4 GlyAlaGlyAlaAlaArgGlyArgAlaSerTrpCysTrpAlaLeuAlaLeuLeuTrpLeu GGGGCCGGGGGGCCGGCTGTTCGTGGGCCTGG----210 67.00 54.17% 54.17% 43.51% ABZ96032 (1-2028) Mismatches: Indels: Conservative: Matches: 2028 13 0 9 2 -GGGTGCCTGTGGCTG

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'command line parameters:
'MODEL=frame+ p2n.model -DEV=xlh
'MODEL=frame+ p2n.model -DEV=xlh
'O=/cgn2_1/USFTO_Spool/US10010050/runat_22042004_113204_27556/app_query.fastz_1.1372
'DB=EST -QFMT=fastap -SUPFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
'UNITS=bits -START=1 -END=-1 -WATELX=blosum62 -TRANS=buman40.cdi -LIST=45
'DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -WODE=LOCAL
'OUTFMT=pto -NORM=sext -HBAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
'USER=US10010050 @CGN 1_1 6283 @runat_22042004_113204_27556 -NCPU=6 -ICPU=3
'NO MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
'NO MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
'DEV_TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPDF=10 -XGAPEXT=0.5 -FGAPOP=6
'PGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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SUMMARIES

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ALIGNMENTS

REFERENCE	M.S	VERSION KEYWORDS	ACCESSION	DEFINITION	LOCUS	AL546472	RESULT 1
EUKATYOCA; MECAZOA; CHOTGATA; CTANIACA; VETCEOTATA; EUTELEOSTOMI; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1201)	Homo sapiens (human) Homo sapiens	AL546472.2 GI:31268306 EST.	<pre>clone CS0DI030YJ01 5-PRIME, mRNA sequence. AL546472</pre>	AL546472 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA	AL546472 1201 bp mRNA linear EST 31-MAY-2003		

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cgi-bin/cluster.cgi?seq=CSODI030CE01QP1&cluster=7238.f. Contact
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
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Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence beginned to sequence cluster 7238.f For
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/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR i
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Please visit our web site for further URL:http://genome.gsc.riken.go.jp/URL:http://fantom.gsc.riken.go.jp/
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Analysis of the mouse transcriptome of 60,770 full-length CDNAs
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MetArgArgGlyAlaGlyAlaAlaArgGlyArgAlaSerTrp-----CysTrpAlaLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="mRNA"
/strain="C57BL/GJ"
/db_xref="FANTOM_DB;A730075N08"
/db_xref="MGI:2408405"
                                                                                                                                                                                                                                                                                                                                              /tissue type="cerebellum"
/clone lib="RIKEN full-length
/dev_stage="7 days neonate"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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/clone="A730075N08"
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18 6 (bases 1 to 2433)

19 6 (bases 1 to 2433)

19 8 Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, F., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Fukuda, S., Furuno, M., Hiramoto, K., Hiraoka, T., Hirozane, T., Hayashida, K., Hayatsu, N., Ishi, Y., Itoh, M., Kagawa, I., Kasukawa, T., Kotoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, K., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sagabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M., and Hayashizaki, Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new g Genome Res. 10 (10), 1617-1630 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
                                                              Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokoha Kanagawa 230-0045, Japan (B-mail:genome-res@gsc.riken.go.jp, URL.http://genome.gsc.riken.go.jp/, Tel:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Functional annotation of a full-length mouse Nature 409, 685-690 (2001)
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Sciurognathi; Muridae;
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Please visit our web site for further details.
URL:http://genome.gsc.riken.go.jp/.
URL:http://fantom.gsc.riken.go.jp/.
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MetPheAsnGlnMetAlaLysTrpValLysGlnAspAsnGluThrGlyIleTyrTyrGlu
                                                                                                                      AspAspValHisTrpLysGluAsnGlyThrLeuValGlnValAlaThrIleSerGlyAsn
                                                                                                                                                                                                    ProGluMetAspAlaProPheTrpCysAsnGlnGlyAlaAlaCysPhePheGluGlyIle
                                                                                                                                                                                                                                                              TACACAATTGAGTGGTATGAACTTTTCCAGCTGGGCAACTGTACATTTCCCCCACCTCCGG
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/mol type="mRNAs

/strain="CS7BL/60"

/strain="CS7BL/60"

/db_xref="FANTOM_DB:D730033P03"

/db_xref="MGI:2422937"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                location/Qualifiers
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/clone_lib="RIKEN full-length enriched mouse
/dev_stage="10 days lactation, adult"
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Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y., Nuramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system—384 format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                      Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Komno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genome Res. 10 (10), 1617-1630 (2000)
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Mus musculus adult male olfactory brain cDNA, RIENT full-length
enriched library, clone:6430516P20 product:similar to
CEROID-LIPOPUSCINOSIS NEURONAL PROTEIN 5 (CLN5 PROTEIN) [Homo
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute (Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yoko Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Pax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in R:
Genomic Sciences Center and Genome Science Laboratory in RIKEN
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Analysis of the mouse transcriptome of 60,770 full-length cDNAs
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Please visit our web site for further details.
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SPIPVMKDNIVIEVLALQAPIMEFKYGDLLGHFKLMHDAVGFREKTLTGGKYTILWYEL
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[codon metatr=2]
                                FQLGNCTFPHLRPDKSAPFWCNQGAACFFEGIDDKHWKENGTLSVVATISGNTFNKVA
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NYTKIFLYSGEPIYLGNETSIFGPKGNKTLALAIKKFYGPFRPYLSTKDFLMNFLKIF
                                                                                                                                                                                                                                                                                                                                                                       /note="unnamed protein product; |
similar to CEROID-LIPOFUSCINOSIS
DTVIIHRQFYLFYNFEYWFLPMKPPFVKITYEETPLPTRHTTFTDL'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /dev_stage="adult"
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/clone_Tib="RIKEN full-length enriched mouse
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LysThrLeuSerGlyLeu 346
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                                            CCAATGAAACCCCCCTTTGTCAAAATAACATACGAAGAAACCCCGTTACCCTACCCGACAT
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US-10-010-050A-2 (1-346) x BX331615
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Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSODB009AB01QP1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7238.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
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                                                                                         AAGTATACTTTCTGTCCAACTGGCTCACCTATCCCAGTTATGGAGGGTGATGATGACATT 357
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/db_xref="taxon:9606"
/clone="CS0DB009YC01"
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/mol_type="mRNA"
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CA488543.1
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, N
                                                                                                                                                                                                                                                                                                                                                                                                                                                      mRNA
                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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            /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="texon:9606"
/clone="rMAGE:6720309"
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hTERT-HME1, LNCap"
                                                                                                            Location/Qualifiers
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host="EMDH10B"
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sapiens cDNA clone IMAGE:6720309 5',
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/note="Vector: pCMV-SPORT6; Site_1: EcoRV; Site_2: Not I;
/note="Vector: pCMV-SPORT6; Site_1: EcoRV; Site_2: Not I;
/note="Vector: pcmv-Sport6; Site_1: EcoRV; Site_2: Not I;
/noterior size: 1800 bp. Library maplification: 26,000 fold.
/noterior size: 1800 bp. Library amplification: 26,000 fold.
/noterior size: 1800 bp. Library amplification: 50: 000 fold.
/noterior size: 1800 bp. Library amplification: 26,000 fold.
/noterior size: 1800 b

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Best Local Similarity:
Query Match:
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Plate: LLAM11023 row: a column: 20
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NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health,
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Tissue Procurement: ATCC
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Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
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Technologies."
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CDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LINL at:
http://image.llnl.gov
Plate: LLAM11253 row: n column: 06
High quality sequence stop: 762.
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                                                                                                                                                                                        Contact: Robert Strausberg, l
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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National Institutes of Health, Mammalian
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                   quality sequence stop: ...
Location/Qualifiers
       organism="Homo sapiens"
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                                               le-GluThrAsnTyrThrArg-IlePheLeuTyrSerGly 252
                                                                                                                      AAATCTGTGTTCACGGACCTTTAACAAGTTGGCTGACATTTGGAGCAGAGTTCAAGAACA
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/note="Organ: cervix; Vector: pCMV-SPORT6; Site 1: Not1;
/site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.4 kb. Library prepared by Life
Technologies."
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/tissue_type="cervical carcinoma cell line"
/lab_host="DH10B"
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db_xref="taxon:9606"
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Li, W.B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDM, libraries and normalization Unpublished (2001)
Contact: Genoscope
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BX342662 Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED
Homo sapiens cDNA clone CSODL004YP03 5-PRIME, mRNA sequence.
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BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7238.f
more information about this cluster, see
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Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSODL004CH02QPl.
Location/Qualifiers
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               eGluVaIPheArgLeuGlnAlaProValTrpGluPheLysTyrGlyAspLeuLeuGlyHi
                                                                                                               TAAGTATACTTTCTGTCCAACTGGCTCACCTATCCCAGTTATGGAGGGTGATGATGACAT
                                                                                                                                                      /note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR vsites of the pcMVSPORT 6 vector. Library was normalized
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/cell_line="RAMOS CELL LINE"
/clone_lib="Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED"
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/mol_type="mRNA"
/db_xref="taxon:9606"
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Mammalia; Eutheria; Primates; Ca
1 (bases 1 to 1098)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, N
          CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLN
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM10105 row: g column: 19
                                                                                                                                                                                                                                                                                                                                              BF982158.1 GI:12384970
                                                                                                                                                                                                                                                                                                                                                                              mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                              602308976F1 NIH_MGC_88
                                                                                                                                    Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                    Unpublished (1999)
                                                                                                                                                                                                                                                                                                             Homo
                                                                                                                                                                       Contact: Robert Strausberg, Ph.D
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        AAATT-GTGTCACGGACCTT-AACAAGTTGGCTGAATTTGGAGCAAGATCCAGAACC---
                                       LysPheValLeuArgThrPheAsnLysLeuAlaGluPheGlyAlaGluPheLysAsnlle
                                                                                                                                              <u>AACCAAATGGCAAAGTGGGTGAAACAGGACAATGAAACAGGAATTTATTCTGAGACCTGG</u>
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/tissue_type="duodenal adenocarcinoma, cell line"
/lab_host="DH108 (phage-resistant)"
/clone_lib="WIH MGC 88"
/note="Organ: small_intestine; Vector: pCMV-SPORT6;
Site_1: NotI; Site_2: SalI; Cloned unidirectionally;
oligo-dT primed. Average insert size_1.767 kb. Library
enriched for full-length clones and constructed by Life
Technologies. Note: this is a NIH_MGC Library."
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UI-H-FL1-bgb-i-07-0-UI.81 NCI CGAP FL1 Hc
UI-H-FL1-bgb-i-07-0-UI 3', mRNA sequence.
BU621797
BU621797.1 GI:23288012
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Tissue Procurement: James Martin
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtaine
from Dr. M. Bento Soares, bento-soares@uiowa.edu
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 689)
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National Cancer Institute, Cancer Genome Anatomy Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1997)
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//clone lib="NCI CGAP FIL"

//note="Organ: Chondrosarcoma; Vector: pT7T3-Pac
([Pharmacia] with a modified polylinker; Site 1: BcoR I;
Site 2: Not I; NCI CGAP FIL is a normalized CDNA library
derived from a pool of mRNA obtained from 4 cell lines
from grade III chondrosarcoma tissues. The library was
constructed according to Bonaldo, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA
synthesis was primed with an oligo-dT primer containing a
Not I site. Double stranded cDNA was ligated to an EcoR I
adaptor, digested with Not I, and cloned directionally
into pT7T3-Pac vector. The oligonucleotide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(dT)18 tail. The sequence tag for this library is
GAGGTCGGTG. The cell lines were provided by Dr. James
Martin from the University of Iowa.
TAG TISSUE=Human Chondrosarcoma Grade 3 cell line mix
TAG TISSUE=Human Chondrosarcoma Grade 3 cell line mix
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/lab_host="DH10B (Life Technologies)"
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/tissue_type="Cell lines"
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|mol_type="mRNA"
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                                             Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001)
On Feb 16, 2001 this sequence version replace Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www
                                                                                                                        Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 1201)
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AL571805 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CSODIO30YJO1 3-PRIME, mRNA sequence.
AL571805
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Feng Liang Email: filang&lifetech.com URL:
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSODI030CE01NP1.
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/clone_Tib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/clone_Tib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-cligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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601450425F1 NIH_MGC_65 Homo
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Clone distribution: MGC clone distribution information can
found through the I.M.A.G.B. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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NIH-MGC http://mgc.nci.nih.gov/
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                               AspAspIleGluValPheArgLeuGlnAlaProValTrpGluPheLysTyrGlyAsp
                                                                 LysAsnTyrThrMetGluTrpTyrGluLeuPheGlnLeuGlyAsnCysThrPheProHis 136
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LeuArgProGluMetAspAlaProPheTrpCysAsnGlnGlyAlaAlaCysPhePheGlu
                                                 AAGAACTACACAATGGAATGGTATGAACTTTTCCAACTTGGCAACTGTACATTTCCCCAT
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Location/Qualifiers
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/lab host="DH10B (phage resistant)"
/clone_libe"NIH_MCC_65"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: Not1;
/site_2: Sall; Cloned unidirectionally. Primer: Oligo d'
Average insert size 1.8 kb. Library constructed by Li
Technologies. "
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/db_xref="taxon:9606"
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5', mENA sequence.
CB215456
                                                                                                                                                                                                        Email: cgapbs-r@mail.nih.gov
cDNA Library Preparation:
cDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL
DNA Sequencing by: National Institutes of Health Intram
Sequencing Center (NISC)
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1 (bases 1 to 641)
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Seq primer: M13RP1 reverse primer
                                                                                                                                                                         Clone distribution: NCI-CGAP clone distribution found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg,
                                                                                                                                                                                                                                                                                                                     Unpublished (1997)
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National Cancer Institute, Cancer Genome Anatomy
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                                                                                                                                                                                                                                                                                                                                      Gene Index
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/db_xref="taxon:9606"
/clone="IMAGE:5937013"
                                                                                            Location/Qualifiers
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AGENCOURT 8802804 NIH_MGC_40
5', MRNA sequence.
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                                                                                                                                             GACTGTTCCAAATTTGTGTTAAGGACCTTTAACAAGTTG
                                                                                                                                                                AspCysSerLysPheValLeuArgThrPheAsnLysLeu 230
                                                                                                                                                                                                                  GAGACATGGAATGTAAAAGCCAGCCCAGAAAAGGGGGCAGAGACATGGTTTGATTCCTAC
                                                                                                                                                                                                                                          GluThrTrpAsnValLysAlaSerProGluLysGlyAlaGluThrTrpPheAspSerTyr
                                                                                                                                                                                                                                                                                      AACATGTTCAACCAAATGGCAAAGTGGGTGAAACAGGACAATGAAACAGGAATTTATTAT
                                                                                                                                                                                                                                                                                                              AgnMetPheAsnGlnMetAlaLysTrpValLysGlnAspAsnGluThrGlyIleTyrTyr
                                                                                                                                                                                                                                                                                                                                                          ATTGATGATGTTCACTGGAAGGAAAATGGGACATTAGTTCAAGTAGCAACTATATCAGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AACTACAATGGAATGGTATGAACTTTTCCAACTTGGCAACTGTACATTTCCCCATCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTGGGACACTTGAAAATTATGCATGATGCCATTGGATTCAGAAGTACATTAACTGGCAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GATGACATTGAAGTTTTTCGATTACAAGCCCCAGTATGGGAATTTAAATATGGAGACCTC
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/lab_host="DH10B (T1-resistant)"
/clone_lib="NICHD_HS_Utl"
/clone_lib="NICHD_HS_Utl"
/clone_lib="NICHD_HS_Utl"
/clone_lib="NICHD_HS_Utl"
/clone_unidirection]; Site_1: NotI; Site_2: EcoRV;
Cloned_unidirectionally from microquantity amounts of mRN.
from normal endometrial tissue (late proliferative phase, cycle_day_13). Average insert size 1.9 kb. Library
constructed_by ResGen (Invitrogen Corporation)."
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1 (bases 1 to 974)
NIH-MCC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene
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Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1999)
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                           GlnAlaLysTyrThrPheCysProThrGlySerProIleProValMetGluGlyAspAsp
                                                                                                                                                                                                                                          ArgHisTrpProValProTyrLysArgPheAspPheArgProLysProAspProTyrCys
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                                                                                                                                                                                                                                                                                                                                                                                                                                            GlyAlaGlyAlaAlaArgGly-----ArgAlaSerTrp-----CysTrpAlaLeu
                                                                                                       AspIleGluValPheArgLeuGlnAlaProValTrpGluPheLyaTyrGlyAspLeuLeu
                                                                                                                                                              CAAGCTAAGTATACTTTCTGTCCTACCGGCTCGCCCATCCCAGTTATGAAGGACAATGAC
GGACACTTTAAACTTATGCATGACGCCGTGGGATTCAGGAGCACACTGACAGGCAAGAAC
                             GlyHisLeuLysIleMetHisAspAlaIleGlyPheArgSerThrLeuThrGlyLysAsn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note=Torgan: prostate; Vector: pOTB7; Site_1: XhoI; Site_2: ECORI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5 adaptor: GGCACCAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
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(clsue_type="carcinoma, cell line"
(lash_ost="pH10B (phage-resistant)"
(clone_lib="NIH_MGC_40"
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|db_xref="taxon:9606"
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ACCITITGG
                         GlnPheTyr
                                                                                                       AATTTTATTGGCCCCTTCCAGACCGAATTTGTTCAACCAAAGATTTTCCTGATGAAATTT
                                                                                                                                                         AATGAAACATCTATTTTGGGCCCAAAGGGAACAAGACTTCTGGCCTTTGGCCCATAAAAA 842
                                                                                                                                                                                AsnGluThrSerValPheGlyProThrGlyAsnLysThr-LeuGlyLeuAlaIle-LysA 278
                                                                                                                                                                                                                AAGATAGAAACTATACGAAAATATTTCTTTACAGTGGAGAGCCTATTTACCTGGGA
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                                                                                                                                                                                                                                                                                                                      ACATGGACGGTCCGAGCCCGGCCCAGGACAAGGGGCCCAGACGTGGTTCGAGTCCTACGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCTGACAAGAGCGCTCCCTTCTGGTGTAACCAAGGGGCAGCCTGCTTTTTTGAAGGAATA
                                                                           LeuGln---IlePheAspAlaVal-----
                                                                                                                                rgPheTyrTyrProPheLysProHisLeu---ProThrLysGlu-PheLeuLeuSerLeu
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Search completed: April 25, 2004, 05:45:56 Job time: 4408.8 secs

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=+cgn2_1/USPTO_spcol/US10010050/runat_22042004_113205_27584/app_query.fasta_1.1372
=-published_Applications_NA -CPMT=fastap -SUFFIX=rnpb -MINMATCH=0.1

OPCL=0 -LOODEXX=0 -UNITS=bits -START=1 -END=-1 -MATRIX=bloeum62

RANS=human40.cdi -LIST=45 -DCCALIGN=200 -THR_SCORE=pct -THR_MAX=100

HR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM-ext -HEAPSIZE=500 -MINLEN=0

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TPU=6 -ICPU=3 -NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100

DNGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5

3APOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

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APPLICANT: Sheppard, Paul O.
APPLICANT: Gilbertson, Debra G.
ITITLE OF INVENTION: SECRETED PROTEINS ENCODED BY HUMAN
ITITLE OF INVENTION: CHROMOSOME 13
FILE REFERENCE: 97-38
CURRENT APPLICATION NUMBER: US/09/122,383A
CURRENT FILING DATE: 1998-07-24
EARLIER APPLICATION NUMBER: 60/053,613
EARLIER APPLICATION NUMBER: 60/053,613
EXARLIER FILING DATE: 1997-07-24
NUMBER OF SEQ ID NOS: 19
SOFTMARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 1
US-09-122-383-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
NAME/KEY: CDS
LOCATION: (47)...(1084)
                                                                      ORGANISM: Homo sapien
                                                                                                   TYPE: DNA
                                                       FEATURE:
                                                                                                                      LENGTH:
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RESULT 2
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US-10-010-050A-1
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Best Local Similarity:
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APPLICANT: Sheppard, Paul O.
APPLICANT: Gilbertson, Debra G.
TITLE OF INVENTION: SECRETED PROTEINS ENCODED
TITLE OF INVENTION: CHROMOSOME 13
FILE REFERENCE: 97-38C1
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NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 1
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Publication No. US20020173624A1
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ORGANISM: Homo :
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{\tt MetGluTrpTyrGluLeuPheGlnLeuGlyAsnCysThrPheProHisLeuArgProGlumetGluTrpTyrGluLeuPheGlnLeuGlyAsnCysThrPheProHisLeuArgProGlumetGluTrpTyrGluLeuPheGlnLeuGlyAsnCysThrPheProHisLeuArgProGlumetGluTrpTyrGluLeuPheGlnLeuGlyAsnCysThrPheProHisLeuArgProGlumetGluTrpTyrGluLeuPheGlnLeuGlyAsnCysThrPheProHisLeuArgProGlumetGluTrpTyrGluLeuPheGlnLeuGlyAsnCysThrPheProHisLeuArgProGlumetGluTrpTyrGluLeuPheGlnLeuGlyAsnCysThrPheProHisLeuArgProGlumetGluTrpTyrGluLeuPheGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpTyrGluTrpT
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PRIOR APPLICATION NUMBER: PCT/US99/05804
PRIOR FILING DATE: 1999-03-18
PRIOR PPLICATION NUMBER: 60/078,566
PRIOR PILING DATE: 1998-03-19
PRIOR PRILING DATE: 1998-03-19
PRIOR PPLICATION NUMBER: 60/078,576
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PRIOR PPLICATION NUMBER: 60/078,574
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PRIOR PPLICATION NUMBER: 60/078,574
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PRIOR PRIOR DATE: 1998-03-19
PRIOR PPLICATION NUMBER: 60/078,579
PRIOR PPLICATION NUMBER: 60/078,579
PRIOR PILING DATE: 1998-03-19
PRIOR FILING DATE: 1998-03-19
PRIOR FILING DATE: 1998-04-01
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S-10-653-595-26
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Publication No. US20040048304A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/653,595
CURRENT FILING DATE: 2003-09-03
                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: 95 Human secreted proteins FILE REFERENCE: PZ027P1C1
                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 09/397945
PRIOR FILING DATE: 1999-09-17
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; NAME/KEY: SITE
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US-10-653-595-26
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Query Match:
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PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/078,578
PRIOR FILING DATE: 1998-03-19
Remaining Prior Application data removed
NUMBER OF SEQ ID NOS: 470
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LOCATION: (1735)
OTHER INFORMATION:
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LOCATION: (1689)
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LOCATION: (1557)
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                                            TTGAAAATTATGCATGATGCCATTGGATTCAGAAGTACATTAACTGGCAAGAACTACACA
                                                           LeuLysIleMetHisAspAlaIleGlyPheArgSerThrLeuThrGlyLysAsnTyrThr
                                                                                                  GAAGTTTTTCGATTACAAGCCCCAGTATGGGAATTTAAATATGGAGACCTCCTGGGACAC
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PRIOR APPLICATION NUMBER: PCT/US99/05804
PRIOR FILING DATE: 1999-03-18
PRIOR FILING DATE: 1998-03-19
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/078,576
PRIOR APPLICATION NUMBER: 60/078,576
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/078,573
PRIOR FILING DATE: 1998-03-19
PRIOR FILING DATE: 1998-03-19
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                PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Human Genome Sciences, Inc. et al. TITLE OF INVENTION: 95 Human secreted proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/397,945
CURRENT FILING DATE: 1999-09-17
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                                                             DR APPLICATION NUMBER: 60/078,574
DR FILLING DATE: 1998-03-19
DR APPLICATION NUMBER: 60/078,579
DR FILLING DATE: 1998-03-19
DR APPLICATION NUMBER: 60/080,314
DR FILLING DATE: 1998-04-01
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                APPLICATION NUMBER: 60/080,312
FILING DATE: 1998-04-01
APPLICATION NUMBER: 60/078,578
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PRIOR APPLICATION NUMBER: 60/078,581
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PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/078,563
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PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/080,313
PRIOR FILING DATE: 1998-04-01
NUMBER OF SEQ ID NOS: 470
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GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
APPLICANT: Gilbertson, Debra G.
APPLICANT: Gilbertson, Debra G.
TITLE OF INVENTION: CHROMOSOME 13
TITLE OF INVENTION: CHROMOSOME 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 13, Application UPatent No. US20020042093A1
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-09-122-383-13
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SOFTWARE: FastSEQ for Windows Version
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NAME/KEY: variation
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                                        TAYCCNTTYAARCCNCAYYTNCCNACNAARGARTTYYTNYTNWSNYTNYTNCARATHTTY
                                                        TyrProPheLysProHisLeuProThrLysGluPheLeuLeuSerLeuLeuGlnIlePhe
                                                                                                                  ThrSerValPheGlyProThrGlyAsnLysThrLeuGlyLeuAlaIleLysArgPheTyr
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publication No. US20020173624A1
GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
APPLICANT: Gilbertson, Debra G.
APPLICANT: Gilbertson, Debra G.
TITLE OF INVENTION: SECRETED PROTEINS ENCODED
TITLE OF INVENTION: CHROMOSOME 13
FILE REFERENCE: 97-38C1
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PRIOR FILING DATE: 1998-07-24
PRIOR APPLICATION NUMBER: US 60/053,613
PRIOR FILING DATE: 1997-07-24
NUMBER OF SEQ ID NOS: 19
SOFTMARE: FastSEQ for Windows Version 4.0
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OTHER INFORMATION: n =
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    APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACII
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACII
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT APPLICATION NUMBER: US 60/180,312
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 99/632,366
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 09/632,366
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Publication No. US20040048304A1
GENERAL INFORMATION:
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TITLE OF INVENTION: 95 Human secreted proteins
FILE REFERENCE: PZ027F1C1
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PRIOR FILING DATE: 1999-09-17
PRIOR APPLICATION NUMBER: PCT/US99/05804
PRIOR FILING DATE: 1999-03-18
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                               DR FILING DATE: 1998-03-19
R APPLICATION NUMBER: 60/078,573
DR FILLING DATE: 1998-03-19
DR APPLICATION NUMBER: 60/078,574
DR FILING DATE: 1998-03-19
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Percent Similarity:
Best Local Similarity:
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PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/078,578
PRIOR FILING DATE: 1998-03-19
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CURRENT APPLICATION NUMBER: US/09/397,945
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PRIOR APPLICATION NUMBER: PCT/US99/05804
PRIOR APPLICATION NUMBER: 60/078,566
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PRIOR FILING DATE: 1998-03-19
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IS-09-397-945-26
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Publication No. US20030065139A1
GENERAL INFORMATION:
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FILING DATE: 1998-04-01
APPLICATION NUMBER: 60/078,578
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PRIOR FILING DATE: 1998-03-19
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APPLICANT: Sheppard, Paul O.
APPLICANT: Sheppard, Paul O.
APPLICANT: Gilbertson, Debra G.
APPLICANT: Gilbertson, Debra G.
TITLE OF INVENTION: SECRETED PROTEINS ENCODED BY
TITLE OF INVENTION: CHROMOSOME 13
FILE REFERENCE: 97-38
CURRENT APPLICATION NUMBER: US/09/122,383A
CURRENT APPLICATION NUMBER: 60/053,613
EARLIER APPLICATION NUMBER: 60/053,613
EARLIER FILING DATE: 1997-07-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3-09-122-383-13
                                                                                                                                                                                                         SOFTWARE: FastSEQ for SEQ ID NO 13
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                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 19
                NAME/KEY: variation
LOCATION: (1)...(1038)
OTHER INFORMATION: n i
                                                                                        OTHER INFORMATION:
                                                                                                                               TYPE: DNA ORGANISM: Artificial FEATURE:
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S-10-010-050A-2 (1-346) x US-10-010-050A-13 (1-1038)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/010,050A CURRENT FILING DATE: 2002-03-26 PRIOR APPLICATION NUMBER: US 09/122,383 PRIOR FILING DATE: 1998-07-24 PRIOR APPLICATION NUMBER: US 60/053,613 PRIOR FILING DATE: 1997-07-24 NUMBER OF SEQ ID NOS: 19
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APPLICANT: Gilbertson, Debra G.
TITLE OF INVENTION: SECRETED PROTEINS ENCODED
TITLE OF INVENTION: CHROMOSOME 13
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                                                                                                                                                                                                                                          TrpProValProTyrLysArgPheAspPheArgProLysProAspProTyrCysGlnAla
                                                                                        GluValPheArgLeuGlnAlaProValTrpGluPheLysTyrGlyAspLeuLeuGlyHis
                                                           GARGINTTYMGNYINCARGCNCCNGTNIGGGARTTYAARTAYGGNGAYYTNYINGGNCAY
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     APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACII
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACII
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACII
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACII
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ANALYSIS BY MICROARRAY
FILE OF INVENTION NUMBER: US 60/180,312
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR PILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR PILING DATE: 2000-10-04
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OTHER INFORMATION: MAP TO ACOO1226.1

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 4.5

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 6.3

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 5.6

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 5.6

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.6

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.9

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 4.2

OTHER INFORMATION: MT HIT: 915729771, EVALUE 0.00e+00

OTHER INFORMATION: SWISSPROT HIT: 075503, EVALUE 2.00e-96

OTHER INFORMATION: EST_HUMAN HIT: H01255.1, EVALUE 0.00e+00
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FILING DATE: 2001-01-30
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APPLICATION NUMBER: PCT/US01/00665
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APPLICATION NUMBER: PCT/US01/00669
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APPLICATION NUMBER: PCT/US01/00664
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                           TyrThrArgIlePheLeuTyrSerGlyGluProThrTyrLeuGlyAsnGluThrSerVal
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TATACAAGAATATTTCTTTACAGTGGAGAACCTACTTATCTGGGAAATGAAACATCTGTT
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                             Alignment Scores:
                Pred. No.:
                                                                 US-10-040-739-825
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                                                                                                                                 INFORMATION FOR SEQ ID NO: 825:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 506 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/040,739
FILING DATE: 07-Jan-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Merberg, David
Treacy, Maurice
Spaulding, Vikki
TITLE OF INVENTION: SECRETED,
NUMBER OF SEQUENCES: 1519
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MEDIUM TYPE: Floppy Disk
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                                                                                  TOPOLOGY: linear MOLECULE TYPE: cDNA SEQUENCE DESCRIPTION: SEQ ID
                                                                                                                                                                                                                                                        NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 09/036,520 FILING DATE: 03-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: Massachusetts
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STREET: 87 CambridgePark Drive
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TELEFAX: (617) 8.
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o. US20020173635A1
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PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00669
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st Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
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APPLICANT: Chen, Wensheng
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Pred. No.:
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SOFTWARE: Annomax Sequence I
SEQ ID NO 5832
LENGTH: 474
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ORGANISM: Homo
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OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: PCT/US01/00661
OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: PCT/US01/00670
OR APPLICATION NUMBER: PCT/US01/00670
OR APPLICATION NUMBER: US 60/234,687
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NR APPLICATION NUMBER: US 09

NR FILING DATE: 2000-06-30

NR APPLICATION NUMBER: US 09

NR APPLICATION NUMBER: US 09

NR FILING DATE: 2001-01-29
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                                                                              GlyLeuAlaIleLysArgPheTyrTyrProPheLysProHisLeuProThrLysGluPhe
                                                                                                                                                                                                                                TTTGGAGCAGAGTTCAAGAACATAGAAACCAACTATACAAGAATATTTCTTTACAGTGGA
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I EXPRESSED IN PLACES
I EXPRESSED IN BONE I
EXPRESSED IN ADULT
EXPRESSED IN LUNG,
EXPRESSED IN HELLA,
EXPRESSED IN HEART
EXPRESSED IN HEART
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IN BRAIN, SIGNAL = 6.3
IN BONE MARROW, SIGNAL =
IN ADULT LIVER, SIGNAL = 5
IN LUNG, SIGNAL = 3.6
IN HELA, SIGNAL = 3.9
IN HELAT, SIGNAL = 4.2
IN FETAL LIVER, SIGNAL = 5
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Conservative:
Mismatches:
Indels:
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CURRENT APPLICATION NUMBER: US/10/264,049
CURRENT FILING DATE: 2002-10-04
PRIOR APPLICATION NUMBER: PCT/US01/18569
PRIOR FILING DATE: 2001-06-07
PRIOR APPLICATION NUMBER: US 60/209,467
PRIOR FILING DATE: 2000-06-07
NUMBER OF SEQ ID NOS: 4360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Birse et al. TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PAl33P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      equence 1859, Application US/10264049
ublication No. US20040005579A1
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EQ ID NO 1859
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LOCATION: (323)...(324)
OTHER INFORMATION: n equals
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LOCATION: (313)...(313)
OTHER INFORMATION: n equals
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LOCATION: (285)...(285)
OTHER INFORMATION: n equals
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OTHER INFORMATION: n equals
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LOCATION: (175)..(175)
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LOCATION: (2)...(2)
OTHER INFORMATION: n equals
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LOCATION: (331)...(331)
OTHER INFORMATION: n equals
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LOCATION: (295)..(295)
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LOCATION: (395)...(395)
OTHER INFORMATION: n equals
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FEATURE:
NAME/KEY: misc_feature
LOCATION: (483)..(483)
OTHER INFORMATION: n equals
                                                                         NAME/KEY: misc feature LOCATION: (478)...(478) OTHER INFORMATION: n equals
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LOCATION: (464)..(464)
OTHER INFORMATION: n equals
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LOCATION: (458)...(458)
OTHER_INFORMATION: n equals
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LOCATION: (440)...(440)
OTHER INFORMATION: n equals
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APPLICANT: Jones, Robert
APPLICANT: Jones, Robert
APPLICANT: Jones, Robert
APPLICANT: Harlocker, Susan L.
APPLICANT: Harlocker, Susan L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
TITLE REFERENCE: 210121.497
FILE REFERENCE: 210121.497
CURRENT APPLICATION NUMBER: US/09/867,701
CURRENT APPLICATION AUMBER: US/09/867,701
CURRENT APPLICATION AUMBER: US/09/867,701
CURRENT FILING DATE: 2001-05-29
NUMBER OF SEQ ID NOS: 10912
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2579
LENGTH: 351
TYPE: DNA
TYPE: DNA
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Best Local Similarity:
Query Match:
DB:
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GC-TGCTTTTTTGAGGGAATTGATGATGTTCACTGGAAGGAAAATGGGACATTAGTTCAA
                                                                             CysThrPheProHisLeuArgProGluMetAspAlaProPheTrpCysAsnGlnGlyAla 151
                                                                                                                                  SerThrLeuThrGlyLysAsnTyrThrMetGluTrpTyrGluLeuPheGlnLeuGlyAsn
                   AlaCysPhePheGluGlyIleAspAspValHisTrpLysGluAsnGlyThrLeuValGln
                                                         TGTACATTTCCCCATCTCCGACCTGAAATGGATGCCCCTTTCTGGTGTAATCAAGGCGCT
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SOFTWARE: PatentIn version 3.0
SEQ ID NO 1363
LENGTH: 473
TYPE: DNA
ORGANISM: Homo sapiens
IS-09-954-456-1363
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PRIOR FILING DATE: 2000-09-20
PRIOR APPLICATION NUMBER: US/60/234,923
PRIOR FILING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: US/60/235,134
PRIOR FILING DATE: 2000-09-25
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NUMBER OF SEQ ID NOS: 2276
                                                                                                                                                                                                                                                                              No.:
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FILING DATE: 2000-09-26
APPLICATION NUMBER: US/60/235,638
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FILING DATE: 2000-09-27
APPLICATION NUMBER: US/60/235,720
FILING DATE: 2000-09-27
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                                                                                             | LyspheProPheIleLysIleThrTyrGluGluIleProLeuProIleArgAsnLysThr 342
                                                                      GTGATTGTGCACAAACAGTTCTATTTGTTTTATAATTTTGAATATTGGTTTTTACCTATG
AAATTCCCCTTTTATTAAAATAACATATGAAGAAATCCCTTTACCTATCAGAAACAAAACA
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100.00%
12.51%
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APPLICANT: FAIGLER, Simchon
TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE VEILE REFERENCE: 36688-005
CURRENT APPLICATION NUMBER: US/09/908,975
CURRENT FILLING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: US 60/287,724
PRIOR FILING DATE: US 60/287,724
PRIOR APPLICATION NUMBER: US 60/287,724
PRIOR PILING DATE: 2000-05-02
PRIOR PILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 32337
SOFTWARE: Patentin version 3.0
SEQ ID NO 10339
LENGTH: 60
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US-09-908-975-10339
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APPLICANT: Wang, Youzhen
APPLICANT: Steinmann, Kathleen
TITLE OF INVENTION: FOR IDENTIFICATION, ASSESMENT, PRE
TITLE OF INVENTION: THERAPY OF BREAST CANCER
FILLE REFERENCE: MRI-049
CURRENT APPLICATION NUMBER: US/10/198,846
CURRENT FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/306,220
PRIOR TILING DATE: 2001-07-18
PRIOR APPLICATION NUMBER: 60/306,220
PRIOR TILING DATE: 2001-07-18
PRIOR TILING DATE: 2001-07-18
PRIOR APPLICATION NUMBER: 60/306,220
PRIOR TILING DATE: 2001-07-18
PRIOR FILING DATE: 2001-07-18
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US-09-908-975-10339
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US-10-198-846-9753
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                              LENGTH: 2667

TYPE: DNA
ORCANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: 2667
OTHER INFORMATION: n = A,T,C o.
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er 33 CCG 173.7 50 64 CC 1618 CC 1618 CC 1618 CC 1493 TTC 14	N 4	שי	;	о <u>н</u> к	11.	CAGC 116	122	C 128	LeuArgProGlu 140 ::: ACCAGCCCCAAA 134	14	145	80 149	- 68 T 155	161	- 50 A 16	20 LeuLeuTrpLeuAlaValValProGlyTrpSerArgValSer 33	10-010-050A-2 (1-346) x US-10-198-846-9753 (1-2667)	gnment Scores: 0.00739 Length: 2667 d. No.: 112.00 Matches: 84 re: 112.00 Matches: 36 cent Similarity: 32.17% Conservative: 36 restriction: 12.1 12.1 it Local Similarity: 22.52% Mismatches: 12.1 Indels: 13.3 Indels: 13.3 Gaps: 19
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APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Gladman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Gen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN
TITLE OF INVENTION: DALANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
FURRENT APPLICATION NUMBER: US(10/369,493)
CURRENT APPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION NUMBER: US 60/360,039
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US-10-369-493-33507
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Best Local Similarity:
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US-10-369-493-33507
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SEQ ID NO 33507
LENGTH: 3530
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publication No. US20030233675A1
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                                     2493 GTGATTGGAGGAGTGACCAATCTG-
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     117 LysAsn----
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                                                                                                                                                                                                     TyrCysGlnAlaLysTyrThrPheCysProThrGlySerProIleProValMetGluGly 76
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ATGGCTATATTGAGGAAATGATCCATGGCCAGCGGGTGGTCAAGGTCTTCAACTATGAGG 2343
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                                                                                                                                    AspAspAspIleGluValpheArgLeuGlnAlaProValTrpGluPheLysTyrGlyAsp 96
                                                               LeuLeuGlyHisLeuLysIleMetHisAspAlaIleGlyPheArgSerThrLeuThrGly 116
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is derived by analysis of the total score distribution.
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seq length: 2000000000
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2: /cgn2_6/ptodata/2
3: /cgn2_6/ptodata/2
4: /cgn2_6/ptodata/2
5: /cgn2_6/ptodata/2
6: /cgn2_6/ptodata/2
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/BCTUS_COMB.seq:*
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US-09-453-702B-22

US-09-489-039A-6332

US-09-976-594-24

US-08-976-594-73

US-08-290-448A-73

US-08-290-448A-73

US-08-461-939B-73

US-08-461-939B-73

US-08-464-000-73
              US-08-480-528A-11
US-08-479-666-11
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 Sequence 2, Appli
Sequence 22, Appl
Sequence 632, App
Sequence 244, App
Sequence 73, Appl
Sequence 71, Appl
Sequence 11, Appl
Sequence 11, Appl
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US-09-108-006C-2
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2274	2043	1533	438	3577	2166	2166	2166	2166	1890	1575	1398	1368	429	13993		537	5574	5433	5433	5433	5433	4440	4440	4440		12394	1328	1328	1328	1328	1328	3113
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-09-252-991A-934	9-252-991A-	-09-252-991A-937	-09-252-991A-948	-09-620-312D-45/	-09-232-195-10	-09-232-201-10	-09-232-197-10	-09-232-200-10	09-252-991A-633	-09-252-991A-7	-09-252-991A-641	-09-252-991A-717	-09-252-991A-621	-09-220-132-20	-09-976-594-10	-09-134	-09-620-3120-2	-09-591-514-35	-09-023	-09-156-842-35	-09-157	-59	-09-156	-09-157	-07-792	-09-488	8-464	-08-461	-08-175	-290-448A	-08-290-448A	28-272-
934/	9459,	2010	101101	1000	101		1 1	101,	000		equence our	(1 1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	3 6) 	۱ د ۱ د	۱ <u>د</u>) (3 1	rddw 'co actioning	ы и п ()	equence 1,	equence 1,	Sequence 1, Appli	equence 1,	equence in	quence so	equence so	equence 58	equence se	quence 58	equenc

S-09-108-006C-2
S-09-108-006C-2
Sequence 2, Application US/09108006C

APPLICANT: Steer, Clifford J.
APPLICANT: Steer, Clifford J.
APPLICANT: Steer, Clifford J.
APPLICANT: Betsy T.
Bandyopadhyay, Paramita
Roy-Chowdhury, Jayanta
TITLE OF INVENTION: Hepatocellular Chimeraplasty
NUMBER OF SEQUENCES: 62
CORRESPENT ADDRESS: 62
CORRESPENT US ADDRESS: 62
CORRESPENT ON Pheasant Run
STATE: PA
COUNTRY: USA
ZITY: Newtown
STATE: PA
COUNTRY: USA
ZITY: NEWTOWN
STATE: PA
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER READABLE FORM:
APPLICATION NUMBER: US/09/108,006C
FILLING DATE: 30-Un-1992
CLASSIFICATION NUMBER: 60/054,288
FILLING DATE: 05-AUG-1997
APPLICATION NUMBER: 60/064,996
FILLING DATE: 10-NOV-1997
APPLICATION NUMBER: 60/064,996
FILLING DATE: 10-NOV-1997
APPLICATION NUMBER: 60/064,996
FILLING DATE: 11-FEB-1998

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[-10-010-050A-2 (1-346) \times US-09-108-006C-2 (1-14070)]
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ery Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rcent Similarity:
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INFORMATION FOR SEQ ID NO: 2:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: PCT US
FILING DATE: 30-APR-1998
ATTORNEY/AGENT INFORMATION:
NAME: Friebel, Thomas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12075 CTCAGCAGCCTCCCCAGCCGTAGGCAC-----
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TELEPHONE: 215-504-4444
TELEFAX: 215-504-4545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32 ValSerGlyIleProSerArgArgHisTrpProValProTyrLysArgPheAsp-PheAr 51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 29258
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TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                           aAlaCysPhePheGluGlyIleAspAspValHisTrpLysGluAsnGly---ThrLeuVa 17)
                                  uAlaGluPheGlyAlaGluPheLysAsnIleGluThrAsn---TyrThrArgIlePheLe
                                                                                                                                                                                                            pAsnGluThrGlyIleTyrTyrGluThrTrpAsnValLysAlaSerProGluLysGlyAl 210
                                                                                                                                                                                                                                                             AGAAGTGTCTTCAAAGCTGAGAAGAAATCTGCAGGACCATGCTGAGTGGGTTTATCAA-- 12429
                                                                                                                                                                                                                                                                                                   lGlnValAlaThrIleSerGlyAsnMetPheAsnGlnMetAlaLysTrpValLysGlpAs 190
                                                                                   CAGTGGGACCACTGGGACCTACCAA---
                                                                                                                      aGluThrTrpPheAspSerTyrAspCysSerLysPheValLeuArgThrPheAsnLysLe
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GAGTGGAAGGACAAGGCCCAGAATCTGTACCAGGAACTGTTGAC 12548
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Matches:
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                          TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-09-453-702B-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 22, Application US/09453702B
Patent No. 6365723
GENERAL INFORMATION:
APPLICANT: Blattner, Frederick R.
Alignment Scores:
                                                                                                                                                                     TELEFAX: (608) 251-9
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 8.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/453,702B
FILING DATE: 03-Dec-1999
CLASSIFICATION: cUnknown>
PRIOR APPLICATION: CUKNOWN>
                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION UNMBER: 60/110,955
APPLICATION NUMBER: 60/110,955
FILING DATE: 04-DEC-1998
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J.
RECISTRATION NUMBER: 27386
RECISTRATION NUMBER: 27386
REPERBNOCHO NUMBER: 960296.95017
FELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 251-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12549 TCAGGAAGGCCAAGCCAGTTTCCAGGGACTCAAGGATAACGTGTTTGATGGCTTGGTACG 12608
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TITLE OF INVENTION: No. 6365723el Sequences of E. coli 0157
NUMBER OF SEQUENCES: 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 26:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             294 uSerLeuLeuGlnIlePheAspAlaValIleValHisLysGlnPheTyr-------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: WI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Madison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: US
                                                                                                                                    TYPE: nucleic acid
                                                                                                                                                         ENGTH: 4643
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ed. No.: 3.63
ore: 93.00
reent Similarity: 31.38%
st Local Similarity: 20.34%
lery Match: 4.83%
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RESULT 3
US-09-489-039A-6332
; Sequence 6332, Application US/09489039A
; Patent No. 6610836
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                                                                                                                                                     3996 AAAGGGGATGACTTACAAAGTGAATCCTATAAATCAAAAGGATTTACCGCTTCACTGGAA 4055
                                                                                                                                                                                                                                                                                                                                                                                            167 GlyThrLeuValGln--------ValAlaThrIleSerGlyAsnMet 179
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                                                                                   4056 GCTGGATACAAACACAAATTAGCTGAATTT 4085
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                                                                                                          ------PheAsnLysLeuAlaGluPhe 233
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193 rolyTieTyriyrsinthip	tPhe TTTT	172 AlaThrIleSer		137 uArgProGluMetAspAlaProPheTrpCysAsnGlnGlyAlaAlaCysPhePheGluGL	123	104 tHisAspAlaIleGlyPheArgSerThrLeuThrGlyLySASHIYETHEREGICTEGICTEGICTEGICTEGICTEGICTATGCCGGTGAAGA	84 greudInAlaProValTrpGinPheLySTyrGiyAspLeueudiyArisLe	64 eCysProThrGlySerProIleProValMetGluGlyAspAspAspAspLicollyClick	51ArgProLys-ProAspProTyrCysGlnAlaLysTyrThrPh	44ProTyrLysArgPheAspPhe	29 TrpSerArgValSerGlyIleProSerArgArgHisTr	Scores: 1.04 Length: 92.00 Matches: wilarity: 31.53% Conservative: Similarity: 21.88% Mismatches: Mismatches: 4.77% Indels: h: Gaps: 4	ORMATION: Gary Breton et. al Gary Breton et. al NVENTION: NUCLEIC ACID AND AMINO ACID NVENTION: PNEUMONIAE FOR DIAGNOSTICS / ENCE: 2709.2004001 ENCE: 2709.2004001 ENCE: 2709.2004001 ENCE: 2000-01-27 LING DATE: 2000-01-27 ILCATION NUMBER: US 60/117,747 NG DATE: 1999-01-29 SEQ ID NOS: 14342 332 SEQ ID NOS: 14342 (Klabsiella pneumoniae Klabsiella pneumoniae
	ABRULLII 173 CGAAGACGCGGCGATGAACTATCG 1190 CGAAGACGCGGCGATGAACTATCG 1207		ThrieuValGinVa 172 : GCGCGGAATAACCTGCAGCATAT 1070						gProLys-ProAspProTyrCysGlnAlaLysTyrThrPh 64			1827 77 34 100 141 23) SEQUENCES RELATING TO KLEBSIELLA AND THERAPEUTICS

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RESULT 4
US-09-976-594-244
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Best Local Similarity:
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SOFTWARE: PERL Program
SEQ ID NO 244
LENGTH: 7718
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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APPLICANT: Buchbinder, Jenny
TITLE OF INVENTION: GENES EXPRESSED IN C3A
FILE REFERENCE: PA-0041 US
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CURRENT FILING DATE: 2001-10-12
                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No.
NAME/KEY: unsure
LOCATION: 6339-6362, 6967-7026
OTHER INFORMATION: a, t, c, g, o)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Homo sapiens
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ATGGATGAGGACTTTTGCAGTCGCCTGAGGGAAGGCATGAGGATGAGAGCTCCTGAGTAC 5622
                              GlyAspAspAspIle--
                                                                  TACGGAGTATTGCTGTGGGAAATCTTCTCCTTAGGTGGGTCTCCATACCCAGGAGTACAA :562
                                                                                                                                                                    TrpProValProTyrLysArgPheAsp-----PheArgProLysProAspProTyrCys 58
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Matches:
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                                                                                                                         Patent No. 5676954
GENERAL INFORMATION:
                                                                                                                                                       Sequence
                       APPLICANT: Rafnar, Thorunn
APPLICANT: Kuo, Mei-chang
TITLE OF INVENTION: Allergenic Proteins From Ragweed and
NUMBER OF SEQUENCES: 93
                                                                                       APPLICANT:
APPLICANT:
       CORRESPONDENCE ADDRESS
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                                                                                                                                           73, Application o. 5676954
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GluLeuPheGlnLeuGlyAsnCysThrPheProHisLeuArgProGluMetAspAlaPro 144
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                                                                       Rogers, Bruce
Klapper, David |
Rafnar, Thorunn
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                                                                                           David G
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                                                                                                                                                             US/08290448A
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AlaGluPheLysAsn

239

234

-ThrTyr 256

4225 242

4285

276

4345 296

4405

----TyrGlu 198

---ATC

ADDRESSEE:

Massachusetts

60 State Street,

suite 510

LAHIVE & COCKFIELD

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INFORMATION FOR SEQ ID NO: 73:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: May 29, 1990
APPLICATION NUMBER: US 07/325
FILING DATE: MATCH 17, 1989
ATTORNEY/AGENT INFORMATION:
NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 02109-1075
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE PO Compati
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REFERENCE/DOCKET NUMBER: IM.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
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JURRENT AFFICA-
JURRENT AFFICA-
PRIOR APPLICATION UNMBER: US 07/529,951
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CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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 178
                                                                 158 IleAspAspValHisTrpLysGluAsnGlyThrLeuValGlnValAlaThrIleSerGly 177
                                                                                                                                                                                                                                            625
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 AsnMetPheAsnGlnMetAlaLysTrpValLysGlnAspAsnGluThrGlyIleTyr---
                                                                                                                                  ArgProGluMetAspAlaProPheTrpCysAsnGlnGlyAlaAlaCysPhePheGluGly 157
                                                                                                                                                                         TCACACGTG--
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                                  GCTGATGACACCCATTATCAAGATAAAGGCATGCTA---
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                                                                                                                                                          COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/290,448A
            PILING DATE: August 15, 1994
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 07/529,951
FILING DATE: May 29, 1990
APPLICATION NUMBER: US 07/325,365
FILING DATE: March 17, 1989
ATTORNEY/AGENT INFORMATION:
NAME: ANY E. Mandragouras
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Kuo, Mei-chang
TITLE OF INVENTION: Allergenic Proteins From Ragweed and Uses
NUMBER OF SEQUENCES: 93
                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
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REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                             STATE:
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                                                                                                                                                                                                                                                                                                                                                                 Boston
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Klapper, David G
Rafnar, Thorunn
                                                                                                                                                                                                                                                                                                                                                                                   E: LAHIVE & COCKFIELD
60 State Street, suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        David G.
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              No.:
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ArgProGluMetAspAlaProPheTrpCysAsnGlnGlyAlaAlaCysPhePheGluGly 157
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GCTATTTTTCTCCCATCCGGGTCTGATCCAGTGCTAACCCCTGAGCAAAAAAGCAGGGATG 1113
                             SerValPheGlyProThrGly---AsnLysThrLeuGlyLeuAlaIleLysArgPheTyr 280
                                                                                                                                                                 ArgThrPheAsnLysLeuAlaGluPheGly-----AlaGluPheLysAsnIleGlu 241
                                                                                                                                                                                                                                                                          GTCGTTAACAACAACTACGACAGATGGGGAACGTACGCCATCGGTGGTAGCTCGGCCCCA
                                                                                                                                                                                                                                                                                                                                             AACATGTTCACCGATCACGTTGACCAAAGAATGCCTAGATGTAGATTTGGGTTTTTCCAA
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                                                                                                ThrAsnTyrThrArgIlePheLeuTyrSerGlyGluProThrTyrLeuGlyAsnGluThr 261
                                                                                                                                                                                                     ACTATACTCAGCCAAGGGAACAGATTCTTCGCCCCCGATGATATCATCAAG-----
                                                                   TGGAGAACAGATAGAGACTTGCTTGAAAATGGT
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Percent Similarity:
Best Local Similarity:
Query Match:
                                                       Score:
                                                                        Pred. No.:
                                                                                     Alignment Scores:
                                                                                                                            US-08-175-069A-73
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Patent No. 5776761
GEMERAL INFORMATION:
APPLICANT: Rogers, Bruce
                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/5

FILING DATE: May 29, 1990

APPLICATION NUMBER: US 07/3

FILING DATE: March 17, 1989

ATTORNEY/AGENT INFORMATION:

NAME: Amy E. Mandragouras

REGISTRATION NUMBER: 36,207
                                                                                                                                                                                                                                                                                   TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FALL. DATA:
CURRENT APPLICATION DATA:
CURRENT TOATION NUMBER: US/08/175,069A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD,
STREET: 60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Klapper, David G. APPLICANT: Rafnar, Thorunn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Kuo, Mei-chang
TITLE OF INVENTION: Allergenic Proteins From Ragweed
                                                                                                                                                                                                MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: IM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: sing
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                                                                                                                                             LOCATION:
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US-10-010-050A-2 (1-346) x
RESULT 8
US-08-461-939B-73
US-08-461-939B-73; Sequence 73, Application US/08461939B; Patent No. 6335019; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                             No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
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LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ENGTH:
                                                                                                                                                                                                           526
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/464,000
FILING DATE: 05-JUN-1995
APPLICATION NUMBER: US 08/290,448
FILING DATE: 15-AUG-1994
APPLICATION NUMBER: US 07/529,951
FILING DATE: 29-MAY-1990
FILING DATE: 29-MAY-1990
FILING DATE: US 07/325,365 FILING DATE: 17-MAR-1989
ATTORNEY/AGENT INFORMATION:
NAME: Amy E. Mandragouras
REGISTRATION UNMBER: 36,207
REFERENCE/DOCKET NUMBER: IMITELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400 TELEFAX: (617)742-421 INFORMATION FOR SEQ ID NO: COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA: COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk SEQUENCE CHARACTERISTICS: 586 GGTGATGCTATAAATGTTGCTGGTAGTTCACAAATATGG 78 AspAspIleGluValPheArgLeuGlnAlaProValTrpGluPheLysTyrGlyAspLeu 97 TGTCCAGGAGGCATGATTAAGTCCAACGATGGTCCACCAATTTTTAAGACAACAAAGTGAT 585 AsnTyrThrMetGluTrpTyrGluLeuPheGlnLeuGlyAsnCysThrPheProHisLeu 137 ATCGACCATTGCTCGCTCAGTAAGGCTTCCGATGGGCTGCTCGATATCACCCTCGGCAGC LeuGlyHigLeuLysIleMetHisAspAlaIleGlyPheArgSerThrLeuThrGlyLys 117 28 State Street Klapper, re Klapper, re Thorum Kuo, Mei-chang VENTION: Methods 1349 base pairs Rogers, Bruce (617) 742-4214 LAHIVE & COCKFIELD, LLP single 0.96 90.50 32.17% 21.66% 4.70% Protein 93 US-08-461-939B-73 (1-1349) US/08/461,939B 73: Q. IMI-018CNDV Allergen For Treating Conservative: Mismatches: Indels: Length: Matches: ---ThrGlySerProlleProValMetGluGlyAsp Gaps: ting Sensitivity To A Using Peptides Which #1.25 1349 68 33 120 93 Inloude A T Cell Epitope 684 77 624

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RESULT 9
US-08-464-000-73
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APPLICANT: Rogers
APPLICANT: Riapper,
APPLICANT: Rafnar,
APPLICANT: Kuo, Mei
                                                                                                                                                                                                                                                                                                                                               Sequence 73, Application Patent No. 6335020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                           APPLICANT: Kuo, Mei-chang
TITLE OF INVENTION: Allergenic
NUMBER OF SEQUENCES: 93
                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD,
                                                                         COUNTRY: USA
ZIP: 02109-1875
                                                                                                                                 CITY: Boston
                                                                                                                                                       STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCTATTTTTCTCCCATCCGGGTCTGATCCAGTGCTAACCCCTGAGCAAAAAGCAGGGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ArgThrPheAsnLysLeuAlaGluPheGly-----AlaGluPheLysAsnIleGlu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ServalPheGlyProThrGly---AsnLysThrLeuGlyLeuAlalleLysArgPheTyr 280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----AAAAATGTCTTAGCGAGGACTGGTACTGGCAACGCAGAGTCGATGTCGTGGAAC
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                                                                                                                 Massachusetts
                                                                                                                                                     60 State Street
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Klapper, David G.
Rafnar, Thorunn
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                                                                                                                                                                                                                                 Peptides from Ragweed Pollen
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Best Local Similarity:
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NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: IMI-
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (617)227-594: INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08
FILING DATE: 15-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/464,000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
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                                                                                                                                                                                                                                                                                                                 138 ArgProGluMetAspAlaProPheTrpCysAsnGlnGlyAlaAlaCysPhePheGluGly
                                                                                                                                                                                                                                                                                                                                                                                                                                   625 ATCGACCATTGCTCGCTCAGTAAGGCTTCCGATGGGCTGCTCGATATCACCCTCGGCAGC 684
                                                 856
                                                                                                                                                                                                                                     158 IleAepAspValHisTrpLysGluAsnGlyThrLeuValGlnValAlaThrIleSerGly 177
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                                               GTCGTTAACAACAACTACGACAGATGGGGAACGTACGCCATCGGTGGTAGCTCGGCCCCA 915
                                                                                                                           AACATGTTCACCGATCACGTTGACCAAAGAATGCCTAGATGTAGATTTTGGGTTTTTTCCAA
                                                                                                                                                             AsnMetPheAsnGlnMetAlaLysTrpValLysGlnAspAsnGluThrGlyIleTyr---
                                                                                                                                                                                                       GCTGATGACACCCATTATCAAGATAAAGGCATGCTA-
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90.50
32.17%
21.66%
4.70%
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                                                                                     TyrGluThrTrpAsnValLysAlaSerProGluLysGlyAlaGlu
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           -TrpPheAspSerTyrAspCysSerLysPheValLeu 224
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Matches:
Conservative:
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Indels:
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US-08-480-528A-11
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: PATENT PC-DOS/MS-DOS

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Vi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No. 5652118
GENERAL INFORMATION:
                                                                                                                     INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: PANG, ROY H.L.
APPLICANT: COHEN, CHARLES M.
TITLE OF INVENTION: OP3-INDUCED MORPHOGENESIS
NUMBER OF SEQUENCES: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                       SEQUENCE CHARACTERISTICS:
LENGTH: 6418 base pairs
TYPE: nucleic acid
                                                                                                                                                                                      NAME: FENTON ESQ., GILLIAN M.
REGISTRATION NUMBER: 36,508
REFERENCE/DOCKET NUMBER: CRP-076FW
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/480,528A FILING DATE: 07-JUN-1995 CLASSIFICATION: 435
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KUBERASAMPATH, THANGAVEL
RUEGER, DAVID C.
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Patent No. 56523
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COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/479,666
                                                                                                                                                                                                     APPLICANT: COHEN, CHARLES M.
TITLE OF INVENTION: OP3-INDUCED
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                        STREET: 45 SOUTH
                                                                                                            COUNTRY: UZIP: 01748
                                                                                                                                                                                           ADDRESSEE:
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                                                                                                                                                                            45 SOUTH STREET
                                                                                                                                                                                                                                                       RUEGER, L...
NNG, ROY H.L.
THARLES
                                                                                                                                                                                                                                                                                       OPPERMANN, HERMANN
OZKAYNAK, ENGIN
KUBERASAMPATH, THAN
RUEGER, DAVID C.
                                                                                                                           USA
                                                                                                                                                                                         PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
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                                                                                                                                                                                                                                                                                                         THANGAVEL
                                                                                                                                                                                                                                             MORPHOGENESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAGTCGTGGTGGGTGAAAGAGAGCCTCAA
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                                              US-10-010-050A-2 (1-346) x US-08-479-666-11 (1-6418)
                                                                                     Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                           Pred
                                                                                                                                                        Alignment Scores:
                                                                                                                                                                               ; LOCATION: 6116..63
; OTHER INFORMATION:
US-08-479-666-11
                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: POST FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: 1088..1277
OTHER INFORMATION: /no
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (508) 435-6951
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 6418 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PEATURE:
NAME/KEY: misc_feature
LOCATION: 884..885
OTHER INFORMATION: /note
OTHER INFORMATION: POSTI
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NAME/KEY: exon
LOCATION: 2902..298
OTHER INFORMATION:
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NAME: FENTON Esq., GILLIAN M.
REGISTRATION NUMBER: 36,508
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                                                                                                                                           No.:
                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
NAME/KEY: misc feature
LOCATION: 1834.1835
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NAME/KEY:
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NAME/KEY:
                                                                                                                                                                                                                                                                                       FEATURE:
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CLASSIFICATION:
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OTHER INFORMATION:
                                                                                                                                                                                                                                                            NAME/KEY:
LOCATION:
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LOCATION: 1883..2
OTHER INFORMATION:
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LOCATION: 1350..1814
OTHER INFORMATION: /
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LOCATION: 1..6361
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TCCTGGGCCTGGCGCTATGCG---CGCTGGGCGGGGGGGGGCCCCGGGCCTGCGACCCCCGC 588
                       SerTrpCysTrpAlaLeuAlaLeuLeuTrpLeuAlaValProGly--
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1883..2077
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note=
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                                                                                                                                                                                                                                                                                                                                                                                                          GAP OCCURS BETWEEN
1834 AND 1835 IN THIS SEQUENCE"
                                                                                          Conservative: Mismatches: Indels:
                                                                          Gaps:
                                                                                                                                Length: Matches:
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RESULT 12
PCT-US93-10520-11
                                                                                                                                                                                      Sequence 11, Application PC/TUS9310520 GENERAL INFORMATION:
STREET: 45 U. CITY: HOPKINTON
                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: CREATIVE
                                                                                                                                              TITLE OF INVENTION:
                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1035
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                                                                                                                                                                                                                                                                                                                                                                                            AAGGCAGCCCAGCAGG----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----CTTGAGTGGTGGGTGGC-TGG-----GGGCGGTGGCTCACACCAGCTCTGCCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----AsnGlyThrLeuValGlnValAla-----
                                                         45 SOUTH STREET
                                                                                CREATIVE BIOMOLECULES, INC
                                                                                                                                                 OP3-INDUCED MORPHOGENESIS
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                                                                                                                                                                                                                                                                                                                                                                                              -GAGTCGTGGTGAAAGAGAGCCTCAA 1379
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TELEPHONE: (508)435-9001
INFORMATION FOR SEQ ID NO: 11
SEQUENCE CHARACTERISTICS:
LENGTH: 6418 base pairs
TYPE: nucleic acid
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FILING DATE: 30-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/
FILING DATE: 31-UTL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/
FILING DATE: 31-UTL-1992
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PRIOR APPLICATION NUMBER: US 07/753,059
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 11-MAR-1991
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MEDIUM TYPE: Floppy disk
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TELECOMMUNICATION INFORMATION:
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ATTORNEY/AGENT INFORMATION:
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ZIP: 01748
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LOCATION: 1088..1277
OTHER INFORMATION: //
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OTHER INFORMATION: /not OTHER INFORMATION: Posi
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LOCATION: 1350..1814
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LOCATION:
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LOCATION: 1834..1835
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                             LOCATION: 1883..20 OTHER INFORMATION:
                                                           NAME/KEY: exon
100aTION: 1883..2077
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Positions
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LOCATION:
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OTHER INFORMATION:
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RESULT 13
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; Sequence 58, Application U
; Patent No. 5676554
; GENERAL INFORMATION:
APPLICANT: Rogers, Bru
; APPLICANT: Klapper, Da
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APPLICANT: Origene Technologies
APPLICANT: Origene Technologies
TITLE OF INVENTION: TBX3 GENE AND METHODS
TITLE REFERENCE: 16U 104 R1
CURRENT FILING DATE: 2001-12-28
NUMBER OF SEQ ID NOS: 5
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Klapper, David
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DB:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/290,448A
FILING DATE: AUGUST 15, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/529,951
FILING DATE: May 29, 1990
APPLICATION NUMBER: US 07/325,365
FILING DATE: March 17, 1989
AFTORAMY AGENT INFORMATION:
NAME: AMY E. Mandragouras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: IMI-018CN
TELEPAX: (617)227-7400
TELEFAX: (617)227-7400
TELEFAX: (617)227-5941
TELEPAX: (617)227-5941
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICANT: Kuo, Mei-chang
TITLE OF INVENTION: Allergenic Proteins From Ragweed and Uses
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: cDNA FEATURE:
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ZIP: 02109-1875
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STATE: Massachusetts
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LOCATION:
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TYPE: nucleic acid
STRANDEDNESS: single
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60 State Street, guite 510
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SSULT 15 -08-290-448A-58 Sequence 58, Application US/08290448A Patent No. 5698204 Patent No. 5698204 Patent No. 5698204 Patent No. 5698204 PapulcanT: Risper, David G. AppulcanT: Klapper, David G. AppulcanT: Klapper, David G. AppulcanT: Klapper, Chang TITLE OF INVENTION: Allergenic Proteins From Ragweed and Uses NUMBER OF SEQUENCES: 93 CORRESPONDENCE ADDRESS: ADDRESSE: LAHIVE & COCKFIELD STREET: 60 State Street, suite 510 CITY: Boston STATE: Massachusetts COUNTRY: USA ZIP: 02109-1875 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION NUMBER: US/08/290,448A APPLICATION NUMBER: US/08/290,448A	338 IleargasmiysThrLeu 343 ::: ::: 1255 TTACGTTCAAGTACTCTA 1272	1225 TATTTTATTCCA 1254	318	308PheGluTyr 317	AAGGA 11	289 ThrLysGluPheLeuLeuSerLeuGlnIlePheAspAlaValIleValHisLys 307	81AA	269 AsnLysThrLeuGlyLeuAlaIle	10	15 GACTIG	rArgIlePhe 248	GATAAA 10	95 ACTATACTCAGCCAAGGGAACAGAIICIICGCCCCCGAIGAIGAICAICAICAGCTATACAAG	12	ACAGATGGGGAACGTACGCCATCGGTGGTAGCTCGGCCCCA 8	2	775 AACATGTTCACCGATCACGTTGACCAAAGAATGCCTAGATGTAGATTTGGGTTTTTCCAA 834	178 AsnMetPheAsnGlnMetAlaLysTrpValLysGlnAspAsnGluThrGlyTleTyr 196	724 GCTGATGACACCCATTATCAAGATAAAGGCATGCTAGCAACGGTAGCATTC 774	alGlnVal

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FILING DATE: August 15, 1994

PRIOR APPLICATION NDATA:

APPLICATION NUMBER: US 07/529,951

FILING DATE: May 29, 1990

APPLICATION NUMBER: US 07/325,365

FILING DATE: MARCh 17, 1989

ATTORNEY/AGENT INFORMATION:

NAME: Amy E. MANDER: 36,207

REFERENCE/DOCKET NUMBER: IMI-018CN

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEPAX: (617)227-7400

TELEPAX: (617)227-7400

TELEPAX: (617)227-7400

TELEPAX: (617)227-5941

INFORMATION FOR SEQ ID NO: 58:

SEQUENCE CHARACTERISTICS:
LENGTH: 1128 base pairs
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STRANDEDNESS: single
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Search completed: April 25, 2004, 05:50:25 Job time : 148.853 secs

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Maximum Match 100%
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Abl79601 Human ova
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Human foe
Probe #64
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Human bon
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ALIGNMENTS

AAX02855 standard; DNA; 1486 BP.

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PA (ZY)
                                                                                                                                                                                                                  Secreted protein; zsig46; human; chromosome 13; thyroid; disease; hypothyroidsm; Graves' disease; thyrotoxicosis; thyroid cancer; Hirschsprung's disease; neuronal ceroid-lipofucinosis; Wilson disease; Reiger syndrome; immunoassay; detection; anti-idiotypic antibody; therapy; diagnostic; ss.
                                                                                                                                                                                                                                                                                                 Human zsig46 DNA.
                                                                                                                                                                                                                                                                                                                           14-MAY-1999
                                                                                                                                                                                              Homo sapiens
                         24-JUL-1997;
                                                                             04-FEB-1999
                                                                                                       WO9905275-A1
 (ZYMO ) ZYMOGENETICS INC.
                             97US-0053613P
                                                     98WO-US015431.
                                                                                                                                                      Location/Qualifiers
                                                                                                                                 /product= "zsig46"
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Best Local Si
Query Match:
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Pred. No.:
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cc human protein. The gene number, and the clone it is derived from, are detailed in the descriptor line. The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin Fc portion cc [e.g. AAZ24802] for increasing the stability of the fused protein as cc compared to the human protein only. The invention relates to 95 novel genes and their fragments (nucleic acid sequences: AAZ24811-Z24907; amino cc acid sequences AAY41308-Y41404) which are useful for preventing, treating cc or ameliorating medical conditions e.g. by protein or gene therapy. Also, cc pathological conditions can be diagnosed by determining the amount of the new polymentes in a sample or by determining the presence of mutations cc in the new polymelectides. Specific uses are described for each of the polymenclectides, based on which tissues they are most highly expressed in (see AAZ24811 for described uses)
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                                                                                                                                                                                                                                                                Reiger syndrome; immunoassay; detection; anti-idiotypic
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          New secreted polypeptide, zmig46, and its fragments, related fusion proteins - used for diagnosis and treatment of thyroid disorders or diseases involving genes on chromosome 13.
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C This invention describes the isolation of a novel human secreted protein, c zsig46 encoded by a gene on chromosome 13 which is mainly expressed in c the thyroid. This product can be used to study secretion of proteins from c cells and also to treat or prevent deficient expression of zsig46, which c may be associated with thyroid diseases (e.g. hypothyroidism, Graves' c involve genes in the same region of chromosome 13 (e.g. Hirschsprung's c disease, neuronal ceroid-lipofucinosis, Wilson disease and Reiger c syndrome). Antibodies and other binding proteins, are used as immunoassay c reagents to detect zsig46 or cells expressing it, e.g. for assessing thyroid function to produce anti-idiotypic antibodies, for affinity purification of zsig46, to screen expression libraries, to neutralise zsig46 activity, and to deliver toxins, radioisotopes etc. for therapeutic or diagnostic purposes. Agonists of the product can be used to promote growth, differentiation and proliferation of specific cell types, e.g. for treating (extra)thyroid diseases or as additive to cell
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AsnValLysAlaSerProGluLysGlyAlaGluThrTrpPheAspSerTyrAspCysSer
                               AAYCARATGGCNAARTGGGTNAARCARGAYAAYGARACNGGNATHTAYTAYGARACNTGG
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ma T, Nagai
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u S, Otsuki
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clones. 830 CDNA molecules encoding a human protein have been isolated and nuclectide sequences of 5'- and 3'-ends of the CDNA molecules have been determined. Primers for synthesising the full length CDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA

The invention relates to primers for synthesising full

length

CDNA

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Query Match:
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Alignment
Pred. No.:
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                                                                                                              The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is the nucleotide sequence of the 5'-end of a cDNA provided in the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from EPO
                                                                                                                                                                                                                                                                                                                                                                    WPI;
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11-JAN-2000; 2000JP-00118774
02-MAY-2000; 2000JP-00183765
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                                                                                                                                                                                                                                                                                                  Claim
                                                                                                                                                                                                                                                                                                                                                                                               Wakamatsu
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genetic manipulation.
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Nagai K, Kojima
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Matches:
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S, Otsuki T, K
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The present invention relates to human single exon nucleic acid probes (SENP). The present sequence is one such probe. The SENPs are derived from human HeLa cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                 04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
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                                                                                                                                          genome-derived single exon nucleic acid probes useful expression in human cervical epithelial cells.
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2000US-0207456P.
2000US-00608408.
2000US-00632366.
2000US-0234687P.
2000US-0236359P.
2000US-0024263.
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XX O1-F
DT 01-F
DT 01-F
DT WW02
DX Huma
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26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
                                                    30-JAN-2001; 2001WO-US000669
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27-SEP-2000;
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PR 26-MAY-2000; 2000US-02068408.
PR 21-SEP-2000; 2000US-023659P.
PR 21-SEP-2000; 2000US-0236359P.
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27-SEP-2000; 2000US-0234359P.
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genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to single exon nucleic acid probes the present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying ge expression in samples derived from human placenta. The probes are for antenatal diagnosis of human genetic disorders
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                     The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart. The present sequence is one such probe. The probes may be used for predicting, measuring and displaying gene expression in amples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. carddovascular disease, hypertension, cardiac arrhythmias and congenital heart disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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04-FEB-2000; 2000US-0180312P.
26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
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27-SEP-2000;
04-OCT-2000;
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standard;
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21-SEP-2000;
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26-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                   Example 4;
                                                                                                                                                                                                                                                                Sequence 494
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                                                                                                                                                                                            Match:
                                                                                                                                                                                                                                   No.:
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                                       123
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                                                                                                                                                                                                                                                                                                                                                                                                  exon
                                                                                                                      ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULAR DYNAMICS
                                                    LeuArgThrPheAsnLysLeuAlaGluPheGlyAlaGluPheLysAsnIleGluThrAsn
|||||||
                                                                                           AlaSerProGluLysGlyAlaGluThrTrpPheAspSerTyrAspCysSerLysFheVal
                                                                                                                      GCAAAGTGGGTGAAACAGGACAATGAAACAGGAATTTATTATGAGACATGGAATGTAAAA
                                                                                                                                 AlaLysTrpValLysGlnAspAsnGluThrGlyIleTyrTyrGluThrTrpAsnValLys
                                                                              GCCAGCCCAGAAAAGGGGGCAGAGACATGGTTTGATTCCTACGACTGTTCCAAATTTTGTG
TATACAAGAATATTTCTTTACAGTGGAGAACCTACTTATCTGGGAAATGAAACATCTGTT
            TyrThrArgTlePheLeuTyrSerGlyGluProThrTyrLeuGlyAsnGluThrSerVal
                                                                                                                                                                                                                                                                                                                                                                                                                                           Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 19031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; 2000US-0180312P.

; 2000US-0207456P.

; 2000US-0060840B.

; 2000US-00532366.

; 2000US-0234687P.

; 2000US-0234589P.

; 2000US-0236359P.

; 2000US-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       expressed single
                                                                                                                                                                                                                                                                                                                                                                                                  nucleic acid
                                                                                                                                                             (1-346)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         expressed exon; gene expression
lisease; multiple sclerosis; schi
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            probe; microarray;
epilepsy; cancer;
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HESULT 13
HESY44658
LD ABS44658
CX ABS44
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The invention relates to a single exon nucleic acid probe (SENP) (I) for measuring human gene expression in a sample derived from human adult liver, comprising one of 13109 defined nucleotide sequences given in the specification (or complements) fragments). The probe hybridises at high stringency to a nucleic acid molecule expressed in the human adult liver. (I) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be involved in genetic liver diseases such as cirrhosis, hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is associated with coronary heart disease. ABS25011-ABS51005 represent human liver single exon nucleic acid probes of the invention. Note: The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; single exon nucleic acid probe; liver; cirrhosis;
hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-FEB-2003
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21-SEP-2000;
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30-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human liver single exon probe,
                                                                                                                                                                                                                                                                                                                                                                                             Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MOLE-)
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                                                                                                                                                                                                                                                                                                                4.
                                                                                                                                                                                                                                                                                                                                                                  genome-derived single exon nucleic expression in human adult liver.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IleValHisLysGlnPheTyrLeuPheTyrAsnPheGluTyrTrpPheLeuProMetLys
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; 2000US-00608408.
; 2000US-00632366.
; 2000US-0234687P.
; 2000US-0236359P.
; 2000GB-00024263.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           No.:
                                Human; ds; single exon probe; asthma; lung cancer; COPD; ILD; chronic obstructive pulmonary disease; interstitial lung disease; familial idiopathic pulmonary fibrosis; neurofibromatosis; tuberous sclerosis; Gaucher's disease; Niemann-Pick disease; tuberous sclerosis; Gaucher's disease; Niemann-Pick disease; pulmonary histocytosis; lymphangioleiomyomtosis; karagener syndrome; pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia; primary ciliary dyskinesis; pulmonary hypertension; primary ciliary dyskinesis; pulmonary hypertension;
                                                                                                                                                                                             ABS19237;
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                         hyaline membrane
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                                                                                                                                            genome-derived single exon probe ORF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCAAAGTGGGTGAAACAGGACAATGAAACAGGAATTTATTATGAGACATGGAATGTAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AlaLysTrpValLysGlnAspAsnGluThrGlyIleTyrTyrGluThrTrpAsnValLys
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTTGGGCCAACAGGAAACAAGACTCTTGGTTTAGCCATAAAAAGATTTTATTACCCCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PheGlyProThrGlyAsnLysThrLeuGlyLeuAlaIleLysArgPheTyrTyrProPhe
                                                                                                                                                                                                                     standard;
                                                                                                                                                                                                                                                                   TCTGGTTTA 491
                                                                                                                                                                                                                                                                                             SerGlyLeu 346
                                                                                                                                                                                                                                                                                                                   TTCCCTTTTATTAAAATAACATATGAAGAAATCCCTTTACCTATCAGAAACAAAACACTC
                                                                                                                                                                                                                                                                                                                                    ATTGTGCACAAACAGTTCTATTTGTTTTATAATTTTGAATATTGGTTTTTTACCTATGAAA
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Complements or the 12387 open reading frames derived from the 12087 complements or the 12387 open reading frames derived from the novel set of probes which hybridise at high stringency to a nucleic CC acid expressed in the human lung; measuring the novel set of probes CC early defrom human lung; comprising (a) contacting the array with a CC early; identifying exons in a eukaryotic genome, comprising (a) care and (b) measuring the label detectably bound to each probe of the CC array; identifying exons in a eukaryotic genome, comprising (a) algorithmically predicting at least one exon from genomic sequences of CC the eukaryote; and (b) detecting specific hybridisation of detectably CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe in the above mentioned microarray; assigning exons to a single exon probe comprising (a) identifying exons from genomic sequence by the method above and (b) measuring the expression of each of the exons in several CC tissues and/or cell types using hybridisation to a single exon from expression of the exons in several CC expression of the exons in the tissues and/or cell types using hybridisation to a single exon of 12011 sequences, mentioned in the specification, or encoded by the CC expression of for identifying exons in a gene, particularly using human CC expression and for identifying exons in a gene, particularly using human CC expression, familial idiopathic pulmonary disease (OCPD), interstitial lung cancer, chronic obstructive pulmonary disease (OCPD), interstitial lung cancer, chronic obstructive pulmonary disease (OCPD), interstitial lung cancer, chronic obstructive pulmonary haemosiderosis, pulmonary colliarly cC dyskinesis, pulmonary hypertension and hyaline membrane disease. The probes are sequence is a single exon probe open reading frame of the companies of the printed specification, but was obtained in electronic format directly formation. In the specification, but was obtained in electronic format directly formations.
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27-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nucleic acid probes for measuring gene expression in a sample derived from human lung comprising single exon nucleic acid probes having one 12614 nucleic acid sequences mentioned in the specification, or their complements or the 12387 open reading frames derived from the 12614
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    494 BP;
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  170 A;
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Percent Similarity: Best Local Similarity: Query Match:

886.00 100.00% 100.00% 45.98% 2.45e-84

Conservative: Mismatches:

Alignment

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                                                                                          Jacobs K,
Spaulding
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New polynucleotides encoding human secreted
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IS-10-010-050A-2 (1-346) x AAV88347 (1-506)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               human blood, kidney, foetal lung, placenta, testes, brain, ovary, pituitary, retina and colon cDNA libraries.
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     TTTCTTTACAGTGGAGAACCTACTTATCTGGGAAATGAAACATCTGTTTTTGGGCCAACA
                                                                                                                 <u>AACAAGTTGGCTGAATTTGGAGCAGAGTTCAAGAACATAGAAACCAACTATACAAGAATA</u>
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/db_xref="taxon:9606"
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/note="lat strand cDNA was primed with a NotI-oligo(dT)
/note="lat strand cDNA was primer. Five prime end enriched, double-strand cDNA was
primer. Five prime end enriched, double-strand cDNA was
grimer. Five prime end cloned into the Not I and EcoR V
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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Pred. No. 1.2e-199;
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BX331615 Homo sapiens NEUROBLASTOMA COT 10-NORMALIZED Homo sapiens
cDNA clone CS0DB009YC01 5-PRIME, mRNA sequence.

BX331615 EX331615
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BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7238.f
more information about this cluster, see
                                                                                                            14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Li, W.B., Gruber, C., Jessee, J. and Polayes, D. Full-Length cDNA libraries and normalization Unpublished (2001)
Contact: Genoscope
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Mammalia; Eutheria;
1 (bases 1 to 923)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           cgi-bin/cluster.cgi?seq=CS0DB009AB01QP1&cluster=7238.f. Contact Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InVitroGen Corporation 1600 Faraday Avenue Genoscope sequence ID : CSODB009AB01QP1.
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/clone Tib="Homo sapiens NEUROBLASTOMA COT 10-NORMALIZED"
/clone Tib="Homo sapiens NEUROBLASTOMA COT 10-NORMALIZED"
/clone Tib="Homo sapiens NEUROBLASTOMA COT 10-NORMALIZED"
/note="Tist strand cDNA was primer. Five prime end enriched, double-strand cDNA was
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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/db_xref="taxon:9606"
/clone="CS0DB009YC01"
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96.8%;
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Pred. No. 4.2e-167;
9; Mismatches 18;
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Contact: Genoscope
Genoscope - Centre National de Sequencage
HP 191 91006 EVRY cedex - France
HP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7238.f
more information about this cluster, see
                                                                                             Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vert.
Mammalia; Eutheria; Primates; Catarrhini; Ho!
1 (bases 1 to 1077)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-Length cDNA libraries and normalization
Unpublished (2001)
                                                                                                                                                                                                                                                       BX342662 1077 bp mRNA linear EST 02-N
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Homo sapiens cDNA clone CSODL004YP03 5-PRIME, mRNA sequence.
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501 432 441 372 381

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621 552 561

681

801 732 741 672

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http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODLO04CH02QP1&cluster=7238.f. C
reng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ InVitroGen Corporation
Faraday Avenue Genoscope sequence ID: CSODLO04CH02QP1.
Location/Qualifiers
                                                                         /note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."
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/cell type="B CELLS (RAMOS CELL I
/cell line="RAMOS CELL LINE"
/clone_lib="Homo Bapiens B CELLS
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CA488543 AGENCOURT_10808884 MAPCL Homo sapiens cDNA clone IMAGE:6720309 5', mRNA sequence. CA488543 CA488543.1 GI:24950702 EST: Homo sapiens (human) Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 924) NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mational Institutes of Health, Tissue procurement: Kristi A. Egland, Ira Pastan CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation	738 AGTTGGCTGAACTTGGGAGCACAGTTCAAGAACATTAGAAACCAANTATACAAGAATATT 797 738 AGTTGGCTGAACTTGGGAACCTACTTATCTGGGAAATGAAACATCTGTTTTTTGGGCCAAC 846 790 TCTTTACAGTGG-AGAACCTACTTATCTGGGAAATGAAACATCTGTTTTTTGGGCCAAC 846 798 TCTTTACAGTGGAAGAACCTACTTATCTGGGAAAATGAAACCATCTGTTTAGGGGCAACC 857 847 AGGAAACAAGAC 858		434 GGCAACTGTACATTTCCCCATCTCCGACCTGAAATGGATGCCCCTTTCTGGTGTAATCAA 493	TCCCGGGTCTCGGGCATCCCCTCCCGGCGCACTGGCCGGTGCCCTACAAGCGCTTTGAC TTCCGTCCAAAACCTGATCCTTATTGTCAAGCTAAGTATACTTTCTGTCCAACTGGCTCA TTCCGTCCAAAACCTGATCCTTATTGTCAAGCTAAGTATACTTTCTGTCCAACTGGCTCA TCCGTCCAAAACCTGATCCTTATTGTCAAGCTAAGTATACTTTCTGATCAAGCCCCAGTA CCTATCCCAGTTATGGAGGGTGATGATGAAGTTTTATGGATTACAAGCCCCAGTA CCTATCCCAGTTATGGAGGGTGATGATGAAGTTTTTTCGATTACAAGCCCCAGTA TCGGAATTTAAATATGGAGGGTGATGATCATTGAAGTTTTTTCGATTACAAGCCCCAGTA TGGGAATTTAAATATGGAGACCTCCTGGGACACTTGAAAATTATGCATGATGCCATTGGA TGGGAATTTAAATATGGAGACCTCCTGGGACACTTGAAAATTATGCATGATGCCATTGGA TGGGAATTTAAATATGGAGACCTCCTGGGACACTTGAAAATTATGCATGATGCCATTGGA TGGGAATTTAAATATGGAGACCTCCTGGGACACTTGAAAATTATGCATGATCCAACTT TCAGAAAGTACATTAACTGGCAAGGAACTACACAATGGAAATGGTATGAACTTTTCCAACTT TTCAGAAGTACATTAACTGGCAAGGAACTACACAATGGAATGGTATGAACTTTTTCCAACTT TTCAGAAGTACATTAACTGGCAAAGAACTACACAATGGAATGGTATGAACTTTTTCCAACTT TTCAGAAGTACATTAACTGGCAAAGAACTACACAATGGAATGGTATGAACTTTTTCCAACTT

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Subtracted with brain, liver, lung, kidney and muscle.
Subtracted with brain, liver, lung, kidney and muscle.
Directionally cloned. Priming method: oligo-dT. Average insert size: 1800 bp. Library amplification: 26,000 fold.
Kristi A. Egland, James J. Vincent, Robert Strausberg,
Bungkook Lee & Ira Pastan: Discovery of new breast cancer genes encoding membrane and secreted proteins.
Manuscript submitted."
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Tissue Procurement: ATCC
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                                                                                     Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
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/db xref="taxon:9606"
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/clone="MMGE:4400298"
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/tissue_type="duodenal adenocarcinoma, cell line"
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/clone_lib="N1H MGC 88"
/clone_lib="NCMV-SPORT6;
/note="Organ: small intestine; Vector: pCMV-SPORT6;
/note="Organ: small intestine; Vector: pCMV-
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                                              Nature 420, 563-573 (2002)

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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
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Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Physical and Chemical Research (RIKEN), Laboratory
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Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohar Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome-gsc.riken.go.jp/, Tel:81-45-503-9222, Pax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group Genomic Sciences Center and Genome Science Laboratory in R Division of Experimental Animal Research in Riken contribu prepare mouse tissues.

Please visit our web site for further details.
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/strain="C57BL/6J"
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/clone_Tib="RIKEN_full-length_enriched_mouse_cDNA_library"
/dev_stage="7_days_neonate"
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                         Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishihe, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, B., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y., Okazaki, Y., Sakaya, T., Sakaya, System-384-format
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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E (bases 1 to 2433)

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Adachi, J., Aizawa, K., Akimura, T., Hara, A., Hashizume, W., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiraoka, T., Hirocane, T., Hayashida, K., Hayatsu, N., Hiraoko, K., Hiraoka, T., Kasukawa, T., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, R., Ohno, M., Ohsato, N., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sano, H., Sasaki, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

Direct Submission

Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Functional
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Group Phase I & II Team.
Analysis of the mouse transcriptome
of 60,770 full-length cDNAs
                                                                                                                                                                                                                                                                                                                                                                    820;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/
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Please visit our web site for further details.
                                                                                                                     TRESCTICGCGGTGGTTCCGGGCTGGTCCCGGGGATCCCCTCCCGGCGCCACTG
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/db xref="FANTOM DB:D730033P03"
/db xref="MGI:2422937"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="similar to CEROID-LIPOFUSCINOSIS NEURONAL (CLN5 PROTEIN) [Homo sapiens] (SWISSPROT|075503, FASTY, 73.9%ID, 86.7%length, match=1041)"
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/clone_Tib="RIKEN_full-length_enriched_mouse_cDNA_library"
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Pred. No. 5.7e-138;
0; Mismatches 209;
                                                  -GATTCTGGGCGCGTCCCCGACGTCTGGGCAACGCTG
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Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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1 (bases 1 to 1201)
1 ivases; J. and Polayes; D.
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3 ivases; J. and Polayes; D.
4 ivases; J. and Polayes; D.
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BP 191 91006 EVRY cedex - France
Bmail: segref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7238.f
more information about this cluster, see
                                                                                                                                                                                                                                                                                                                                                                                                           665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    837
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                                      ACAGGAAACAAGACTCTTGGTTTAGCCATAAAAAGATTTTATTACCCCTTCAAACCACAT 904
                                                                                                  <u>ATATTTCTTTÁCAGTGGAGAACCTACTTATCTGGGAAATGAAACATCTGTTTTTGGGCCA</u>
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Location/Qualifiers
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/clone Tib="Homo sapiens PIACENTA COT 25-NORMALIZED"
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/note="ist strand cDNA was primed with a NotI-oligo(dT)
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primer. Five prime end enriched, double-strand cDNA was
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9; Mismatches 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9579 row: b column: 08
High quality sequence stop: 662.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                   /tissue_type="adenocarcinoma"
/tissue_type="adenocarcinoma"
/lab host="0H10B (phage-resistant)"
/clone_lib="NIH_MGC_65"
/note="Torgan: colon; Vector: pCMV-SPORT6; Site_1: Not1;
/note="Torgan: colon; Vector: pCMV-SPORT6; Site_1: Not1;
/site_2: Sall, Cloned unidirectionally. Primer: Oligo dT.
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/db_xref="taxon:9606"
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Pred. No. 9.3e-137;
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                       Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: James Martin
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
seq primer: M13 FORWARD
                                                                                                                                                                                                                   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
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                                                                                                                                                                                                                                                                                                             GGGGGCAGAGACATGGTTTGATTCCTACGACTGTTCCAAATTTGTGTTAAGGACCTTTAA
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                                                                                                                                                                                                        CAAGTTGGCTGAATTTGGAGCAGAGTTCAAGAACATAGAAACCAACTATACAAGAATATT
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               AACTAAAGAATTTCTGTTGAGTCTCTTGCAAATTTTTGATGCAGTGATTGTGCACAAACA
                                                                                           AAACAAGACTCTTGGTTTAGCCATAAAAAGATTTTATTACCCCCTTCAAACCACATTTGCC
                                                                                                                                                                    TCTTTACAGTGGAGAACCTACTTATCTGGGAAATGAAACATCTGTTTTTGGGCCAACAGG
/ clome lib="WGI CGAP FIL"

//clone lib="Grgan: Chondrosarcoma; Vector: pT7T3-Pac

//note="Grgan: Chondrosarcoma; Vector: pT7T3-Pac

//note="Grgan: Chondrosarcoma; Vector: pT7T3-Pac

(pharmacla) with a modified polylinker; Site 1: BcoR I;

Site 2: Not I; NCI CGAP FIL is a normalized cDNA library

derived from a pool of mRNA obtained from 4 cell lines

from grade III chondrosarcoma tissues. The library was

constructed according to Bonaldo, Lemnon and Soares,

Genome Research, 6:791-806, 1996. First strand cDNA

synthesis was primed with an oligo-dT primer containing a

synthesis was primed with an oligo-dT primer containing a

synthesis. Double stranded cDNA was ligated to an EcoR I

adaptor, digested with Not I, and cloned directionally

into pT7T3-Pac vector. The oligonucleotide used to prime

the synthesis of first-strand cDNA contains a library tag

sequence that is located between the Not I site and the

(dT)18 tail. The sequence tag for this library is

GAGGTCGGTG. The cell lines were provided by Dr. James

Martin from the University of Iowa.

TAG TISSUE=Human Chondrosarcoma Grade 3 cell line mix
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/clone="UI-H-FL1-bgb-i-07-0-UI"
/tissue_type="Cell lines"
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AK033293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazzki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDMs to prepare full-length cDMA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
                                                                                                                                                                                                           Group Phase I & II Team.
Analysis of the mouse transcriptome of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 2247)
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Mammalia; Eutheria;
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Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katch, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, R., Ohno, M., Ohsato, N., Nakamura, M., Nishi, K., Nomura, K., Nunazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
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Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
Muramatsu,M. and Hayashizaki,Y.
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Please visit our web site for further details.
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/db_xref="G1:26128113"
/db_xref="G1:26128113"
/translation="LG1ATILGASPTSGORWPUPYKHFSEREKTDPYCOAKYTFCPTG
/translation="LG1ATILGASPTSGORWPUPYKHFSEREKTDRYCOAKYTFCPTG
/translation="LG1ATILGASPTSGORWPUPYKHHDAVGFRSTLTGKNYTIEWYEL
SPIPVMKDNDVLEVLRUQAPIWSFKYGDLLGHFKKNWTLSGNTFNKNYT
PQLGNCTFPHLRPDKSA,PFWCNGGAACFFEGIDDKHWKLRTYKKLABFGTEFKKIT
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EWVKQDNETGIYYETMTVRAGFGGGAGTWFGSYDCSWFYLRTYKKLABFGTEFKKIT
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BX370641 Homo sapiens B
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Full-length cDNA libraries
Unpublished (2001)
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BX370641
                                                                                          Email: segref@genoscope.cns.fr, Web: www.genoscope.cns.fr Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 7238 more information about this cluster, see
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             cgi-bin/cluster.cgi?seq=CSOBAG053ZH03_CS05016_1&cluster=7238.f.
Contact : Feng Liang Email : fliang@llfetech.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSOBAG053ZH03_CS05016_1.
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Mammalia; Eutheria; Primates;
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Faraday Avenue Genoscope sequence
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CELLS (RAMOS CELL LINE) COT 25-NORMALIZED
CSODL004YP03 5-PRIME, mRNA sequence:
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODL004YP03"
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/clone_lib="Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED"
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CB215456.1
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y Match 59.1%; Score 641; DB 14; l
Local Similarity 100.0%; Pred. No. 9.3e-130;
hes 641; Conservative 0; Mismatches 0;
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC)
Clone distribution: NCI-CGAP clone distribution information
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plate: LLAM13163 row: E column: 14
Seq primer: M13RP1 reverse primer (ABI).
Location/Qualifiers
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Unpublished (1997)
Contact: Robert Strausberg,
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 info@image.llnl.gov
Plate: LLAM13163 ro
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National Cancer Institute, Cancer Genome Anat
                                                                                                                                                                                                                                                                            ATGATGACATTGAAGTTTTTCGATTACAAGCCCCAGTATGGGAATTTAAATATGGAGACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="normal endometrium, late proliferative phase, cycle day 13"
/lab host="DH10B (T1-resistant)"
/clome lib="NICHD_HS_Utl"
/clome lib="NICHD_HS_Utl"
/clome lib="NICHD_HS_Utl"
/note="Organ: uterus; Vector: pCMV-SPORT6.1.ccdb (ResGen, Invitrogen Corporation); Site_1: NotI; Site_2: EcoRV; Invitrogen Corporation); Site_1i NotI; Site_2: EcoRV; Cloned unidirectionally from microquantity amount of mRNA from normal endometrial tissue (late proliferative phase, cycle day 13). Average insert size 1.9 kb. Library constructed by ResGen (Invitrogen Corporation)."
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/mol_type="mRNA"
/db_xref="taxon:9606"
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Maximum Match 100%
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1: /cgn2 6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*

2: /cgn2 6/ptodata/1/pubpna/USO6_NEW_PUB.seq:*

3: /cgn2 6/ptodata/1/pubpna/USO6_NEW_PUB.seq:*

4: /cgn2 6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*

5: /cgn2 6/ptodata/1/pubpna/USO7_NEW_PUB.seq:*

6: /cgn2 6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*

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10: /cgn2 6/ptodata/1/pubpna/USO9B_PUBCOMB.seq:*

11: /cgn2 6/ptodata/1/pubpna/USO9E_PUBCOMB.seq:*

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Sequence 13, Appl
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Sequence 22592, A
Sequence 825, App
Sequence 5832, Ap
Sequence 1859, Ap
Sequence 2579, Ap
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ALIGNMENTS

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Sequence 1, Application US/09122383A; Sequence 1, Application US/09122383A; Patent No. US20020042093A1; Patent No. US20020042093A1; Patent No. US20020042093A1; Patent No. US2002004093A1; Patent Separat, Paul O. Applicant: Sheppard, Paul O. Applicant: Sheppard, Paul O. Title OF INVENTION: CHROMOSOME 13; PILE REFERENCE: 97-38; PILE REFERENCE: 97-38; CURRENT APPLICATION NUMBER: US/09/122,383A; CURRENT FILING DATE: 1998-07-24; PARLIER APPLICATION NUMBER: 60/053,613; PARLIER FILING DATE: 1997-07-24; NUMBER OF SEO ID NOS: 19; SOFTWARE: FastSEQ for Windows Version 3.0; SEQ ID NO 1
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ORGANISM: Homo sapien
FEATURE:
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LOCATION: (47)...(1084)
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GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
APPLICANT: Gilbertson, Debra G.
APPLICANT: Gilbertson, Debra G.
TITLE OF INVENTION: SECRETED PROTEINS ENCODED
TITLE OF INVENTION: CHROMOSOME 13
FILE REFERENCE: 97-38C1
CURRENT APPLICATION NUMBER: US/10/010,050A
CURRENT FILING DATE: 2002-03-26
PRIOR APPLICATION NUMBER: US 09/122,383
PRIOR FILING DATE: 1998-07-24
PRIOR APPLICATION NUMBER: US 60/053,613
PRIOR FILING DATE: 1997-07-24
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ORGANISM: Homo sapien
FEATURE:
NAME/KEY: CDS
LOCATION: (47)...(1084)
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PRIOR APPLICATION NUMBER: US 99/397945
PRIOR FILING DATE: 1999-09-17
PRIOR APPLICATION NUMBER: US 99/05804
PRIOR EILING DATE: 1999-03-18
PRIOR APPLICATION NUMBER: 60/078,566
PRIOR APPLICATION NUMBER: 60/078,576
PRIOR PILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/078,574
PRIOR PILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/078,574
PRIOR PILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/078,579
PRIOR APPLICATION NUMBER: 60/078,579
PRIOR APPLICATION NUMBER: 60/078,579
PRIOR APPLICATION NUMBER: 60/080,314
PRIOR PILING DATE: 1998-04-01
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080,312
PRIOR APPLICATION NUMBER: 60/080,312
PRIOR FILING DATE: 1998-04-01
PRIOR PILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080,312
PRIOR APPLICATION NUMBER: 60/080,312
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                                                                                                                                                SOFTWARE: Pa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/653,595
CURRENT FILING DATE: 2003-09-03
                                                                                                                                                                                        Remaining Prior Application data removed NUMBER OF SEQ ID NOS: 470
                                                            ORGANISM: Homo FEATURE:
LOCATION: (1520)
OTHER INFORMATION:
                                                                                                      TYPE: DNA
                                          NAME/KEY: SITE
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APPLICATION NUMBER: 60/078,578
FILING DATE: 1998-03-19
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Matches 1067; Conserv
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RESULT 4
US-09-397-945-26
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CURRENT FILING DATE: 1999-09-17
PRIOR APPLICATION NUMBER: PCT/US99/05804
PRIOR APPLICATION NUMBER: PCT/US99/05804
PRIOR FILING DATE: 1999-03-18
PRIOR FILING DATE: 1999-03-19
PRIOR APPLICATION NUMBER: 60/078,576
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/078,573
PRIOR APPLICATION NUMBER: 60/078,573
PRIOR APPLICATION NUMBER: 60/078,574
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/078,579
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PRIOR FILING DATE: 1998-03-19
PRIOR PILING DATE: 1998-03-19
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TYPE: DNA
TYPE: UNA
ORGANISM: Homo sapiens
FEATURE:
FEATURE:
NAME/KEY: SITE
LOCATION: (1520)
OTHER INFORMATION: n equals a,t,9, o:
NAME/KEY: SITE
LOCATION: (1557)
                                                                                                                                              NUMBER OF SEQ ID NOS: 470
SOFTWARE: PatentIn Ver. 2
SEQ ID NO 26
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                                                                                                                                                                                                               PRIOR
                                                                                                                                  ENGTH:
                                                                                                                                                                                                                                                             OR FILING DATE: 1998-04-01
OR APPLICATION NUMBER: 60/078,578
OR FILING DATE: 1998-03-19
OR PILING DATE: 1998-03-19
OR PILING DATE: 1998-03-19
OR APPLICATION NUMBER: 60/078,577
OR APPLICATION NUMBER: 60/078,577
OR FILING DATE: 1998-03-19
OR FILING DATE: 1998-03-19
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APPLICATION NUMBER: 60/080,313
FILING DATE: 1998-04-01
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